

cryptogamie

Mycologie

2025 • 46 • 5

A new species and a new record for
Pycnoporus P.Karst. (Polyporaceae) from the
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revealed by an integrative approach
of classical taxonomy and phylogenetic studies

Rafaela ARAÚJO F. GURGEL, Catarina S. CARVALHO,
Dirce LEIMI KOMURA, Ruthe DE JESUS SANTOS DALMAN,
Isadora FERNANDES DE FRANÇA,
Ruby VARGAS-ISLA, Noemia KAZUE ISHIKAWA &
Tiara SOUSA CABRAL

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Tian QING

Center of Excellence in Fungal Research, Mae Fah Luang University 333 M. 1 T.Tasud Muang District, Chiang Rai 57100 (Thailand)

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Laboratoire de Botanique, Phytochimie et Mycologie / UMR -CNRS 5175 CEFE, Faculté de Pharmacie, 15, avenue Charles-Flahault, Université Montpellier I, BP 14491, 34093 Montpellier Cedex 5 (France)

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Université de Montpellier II, CEFE/CNRS Campus du CNRS, 1919, route de Mende, 34293 Montpellier Cedex 5 (France)

Naritsada THONGKLANG

Center of Excellence in Fungal Research, Mae Fah Luang University, 333 M. 1 T.Tasud Muang District, Chiang Rai 57100 (Thailand)

Xiang-Hua WANG

CAS Key Laboratory for Plant Diversity and Biogeography of East Asia, Kunming Institute of Botany, Chinese Academy of Sciences, Lanhei Road 132, Kunming 650201, P. R. (China)

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- Science Citation Index
- Publications bibliographiques du CNRS (Pascal)

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- BioOne® (<http://www.bioone.org/loi/crym>)

Cryptogamie, Mycologie est une revue en flux continu publiée par les Publications scientifiques du Muséum, Paris
Cryptogamie, Mycologie is a fast track journal published by the Museum Science Press, Paris

Les Publications scientifiques du Muséum publient aussi / The Museum Science Press also publish: *Adansonia, Geodiversitas, Zoosystema, Anthropolozologica, European Journal of Taxonomy, Naturae, Comptes Rendus Palevol, Cryptogamie* sous-sections *Algologie, Bryologie*.

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diff.pub@mnhn.fr / <http://sciencepress.mnhn.fr>

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ISSN (électronique / electronic): 1776-100

A new species and a new record for *Pycnoporus* P.Karst. (Polyporaceae) from the Brazilian Amazon, revealed by an integrative approach of classical taxonomy and phylogenetic studies

Rafaela ARAÚJO F. GURGEL

Programa de Pós-Graduação em Genética, Conservação e Biologia Evolutiva (PPG GCBEv) do Instituto Nacional de Pesquisas da Amazônia (INPA), Avenida André Araújo, 2936, Petrópolis, 69067-375, Manaus, AM (Brazil)
rafaelaf.gurgel@gmail.com

Catarina S. CARVALHO

Instituto de Pesquisas Jardim Botânico do Rio de Janeiro, Rua Pacheco Leão, 915, 22460-030, Rio de Janeiro, RJ (Brazil)
and Laboratório de Genética e Biologia Reprodutiva de Plantas (LabGen), Programa de Pós-Graduação em Botânica (PPGBot), Instituto Nacional de Pesquisas da Amazônia, Avenida André Araújo, 2936, Petrópolis, 69067-375, Manaus, Amazonas (Brazil)
carvalho_catarina@outlook.com

Dirce LEIMI KOMURA

Instituto Nacional de Pesquisas da Amazônia, Avenida André Araújo, 2936, Petrópolis, 69067-375, Manaus, AM (Brazil)
leimybio@gmail.com

Ruthe DE JESUS SANTOS DALMAN
Isadora FERNANDES DE FRANÇA

Universidade Federal do Pará-Campus Altamira, R. Cel. José Porfírio, Recreio, 68372-040, Altamira, PA (Brazil)
rutheerayran@gmail.com
isadorafranc@ufpa.br

Ruby VARGAS-ISLA
Noemia KAZUE ISHIKAWA

Instituto Nacional de Pesquisas da Amazônia, Avenida André Araújo, 2936, Petrópolis, 69067-375, Manaus, AM (Brazil)
rubyvar9@gmail.com
noemia.kazue@gmail.com

Tiara SOUSA CABRAL

Instituto Nacional de Pesquisas da Amazônia, and Programa de Pós-Graduação em Genética, Conservação e Biologia Evolutiva (PPG GCBEv)-INPA, Avenida André Araújo, 2936, Petrópolis, 69067-375, Manaus, AM (Brazil)
ttiara@gmail.com (corresponding author)

Submitted on 1 July 2024 | Accepted on 8 November 2024 | Published on 3 December 2025

Gurgel R. A. F., Carvalho C. S., Komura D. L., Dalman R.J.S., França, I.F., Vargas-Isla R., Ishikawa N. K. & Cabral T. S. 2025. — A new species and a new record for *Pycnoporus* P.Karst. (Polyporaceae) from the Brazilian Amazon, revealed by an integrative approach of classical taxonomy and phylogenetic studies. *Cryptogamie, Mycologie* 46 (5): 61-86. <https://doi.org/10.5252/cryptogamie-mycologie2025v46a5>. <http://cryptogamie.com/mycologie/46/5>

ABSTRACT

The cosmopolitan genus *Pycnoporus* P.Karst. groups together macrofungi that belong to the family Polyporaceae Fr. ex Corda, and these are identified by the dimidiolate to flabelliform basidiome, coriaceous, reddish-orange, smooth pileus, hymenophore with 3–8 pores per 1 mm, trimitic hyphal system and smooth spores. During a search for poroid fungi of the genus *Pycnoporus* in Brazil, 37 specimens coming from herbaria and 66 recently collected were analyzed. The fungi were analyzed for their macro- and micromorphology, and the ITS, LSU and *tef* regions, which were sequenced and subjected to Bayesian analyses. These analyses showed which characteristics are specific to the genus and new characteristics not previously reported were evidenced. After morphological and phylogenetic analyses, we concluded that some of these specimens were very different from the existing taxa and that they represent a new species of *Pycnoporus*. In addition, *P. puniceus* (Fr.) Ryvarden is reported for the first time from the country and *P. sanguineus* (L.) Murrill from the state of Roraima (Brazil). Furthermore, using the molecular data obtained in this study and ITS, LSU, *tef1* and *rpb2* sequences from Polyporales Gäm. from GenBank, we sought to estimate the time of divergence of *Pycnoporus* and the species on the order, as a starting point for understanding its biogeographic history. According to our analyses, *Pycnoporus* and its sister group *Trametes* Fr. diverged at 36 Mya. Lastly, we discuss the taxonomic relationship between these two groups.

KEY WORDS

Basidiomycota,
cinnabar fungi,
neotropic,
poroid fungi,
polyporales,
Pycnoporus amazonicus,
new species,
new record.

RÉSUMÉ

Une nouvelle espèce et un nouveau signalement de *Pycnoporus* P.Karst. (Polyporaceae) de l'Amazonie brésilienne, révélés par une approche intégrative de la taxonomie classique et des études phylogénétiques.

Le genre cosmopolite *Pycnoporus* P.Karst. regroupe des macrochampignons qui appartiennent à la famille des Polyporaceae Fr. ex Corda et qui sont identifiés par un basidiome dimidié à flabelliforme, un pileus coriace, rouge-orange et lisse, un hyménophore avec 3–8 pores par mm, un système hyphalique trimitique et des spores lisses. Lors d'une recherche de champignons poroïdes du genre *Pycnoporus* au Brésil, 37 spécimens provenant d'herbiers et 66 récemment collectés ont été analysés. Les champignons ont été analysés pour leur macro- et micromorphologie, et séquencés dans les régions ITS, LSU et *tef1*, qui ont été soumises à des analyses bayésiennes. Ces analyses ont montré quelles sont les caractéristiques des espèces du genre, et de nouvelles caractéristiques qui n'avaient pas été signalées auparavant ont été mises en évidence. Après les analyses morphologiques et phylogénétiques, nous avons conclu que certains de ces spécimens étaient très différents des taxons existants et qu'ils représentaient une nouvelle espèce de *Pycnoporus*. En outre, *P. puniceus* (Fr.) Ryvarden est signalé pour la première fois dans le pays et *P. sanguineus* (L.) Murrill dans l'État de Roraima (Brésil). De plus, en utilisant les données moléculaires obtenues dans cette étude et les séquences ITS, LSU, *tef1* et *rpb2* des Polyporales Gäm. de GenBank, nous avons cherché à estimer le temps de divergence de *Pycnoporus* et des espèces de l'ordre, comme point de départ pour comprendre son histoire biogéographique. Selon nos analyses, *Pycnoporus* et son groupe frère *Trametes* Fr. ont divergé à 36 Mya. Enfin, nous discutons de la relation taxonomique entre ces deux groupes.

MOTS CLÉS

Basidiomycota,
champignons cinabres,
néotropiques,
champignons poroïdes,
polyporales,
Pycnoporus amazonicus,
espèce nouvelle,
signalement nouveau.

INTRODUCTION

Pycnoporus P.Karst. is a cosmopolitan genus of the family Polyporaceae Fr. ex Corda (Polyporales Gäm., Basidiomycota R.T. Moore), which was described by Karsten (1881) and currently comprises four species (Nobles & Frew 1962; Lesage-Meessen *et al.* 2011; Gurgel *et al.* 2023). *Pycnoporus palibini* P.Karst. is another reported species (Index Fungorum 2024), but it is absent from taxonomic studies in the genus, probably because its type deposited in the Finnish Museum of Natural History Herbarium-LUOMUS has been re-identified as *Trametes* Fr. The basidiocarp in *Pycnoporus* is reddish-orange colour, generally dimidiolate, with circular to angular pores and trimitic hyphal system; basidiospores are cylindrical, smooth-walled, hyaline and non-amyloid (Ryvarden & Johansen 1980). The genus has a strong phylogenetic relationship with

representatives of the trametoid clade (*Lenzites* Fr. *Coriolopsis* Murril, *Pycnoporus* and *Trametes*), but *Pycnoporus* is a monophyletic group strongly supported by phylogenetic analysis (Lesage-Meessen *et al.* 2011; Welti *et al.* 2012).

In Brazil, the first collection of *Pycnoporus* was recorded more than 250 years ago, along with the history of mycology in the country, when Philibert Commerson collected a specimen of *P. sanguineus* (L.) Murrill near Rio de Janeiro (Fidalgo 1970). For the Brazilian Amazon, the earliest records date back to the 19th century, in 1851 for the present-day municipality of Barcarena (formerly Caripi) in Pará and in 1856 for the community of Panuré (Ipanuré) in Amazonas, collected by Richard Spruce and identified by M. Berkeley (Berkeley 1851, 1856). Since the first record, the species has been reported in different Brazilian phytogeographic domains (Flora do Brasil 2024), and about 1 500 specimens are registered in herbaria (SpeciesLink 2024).

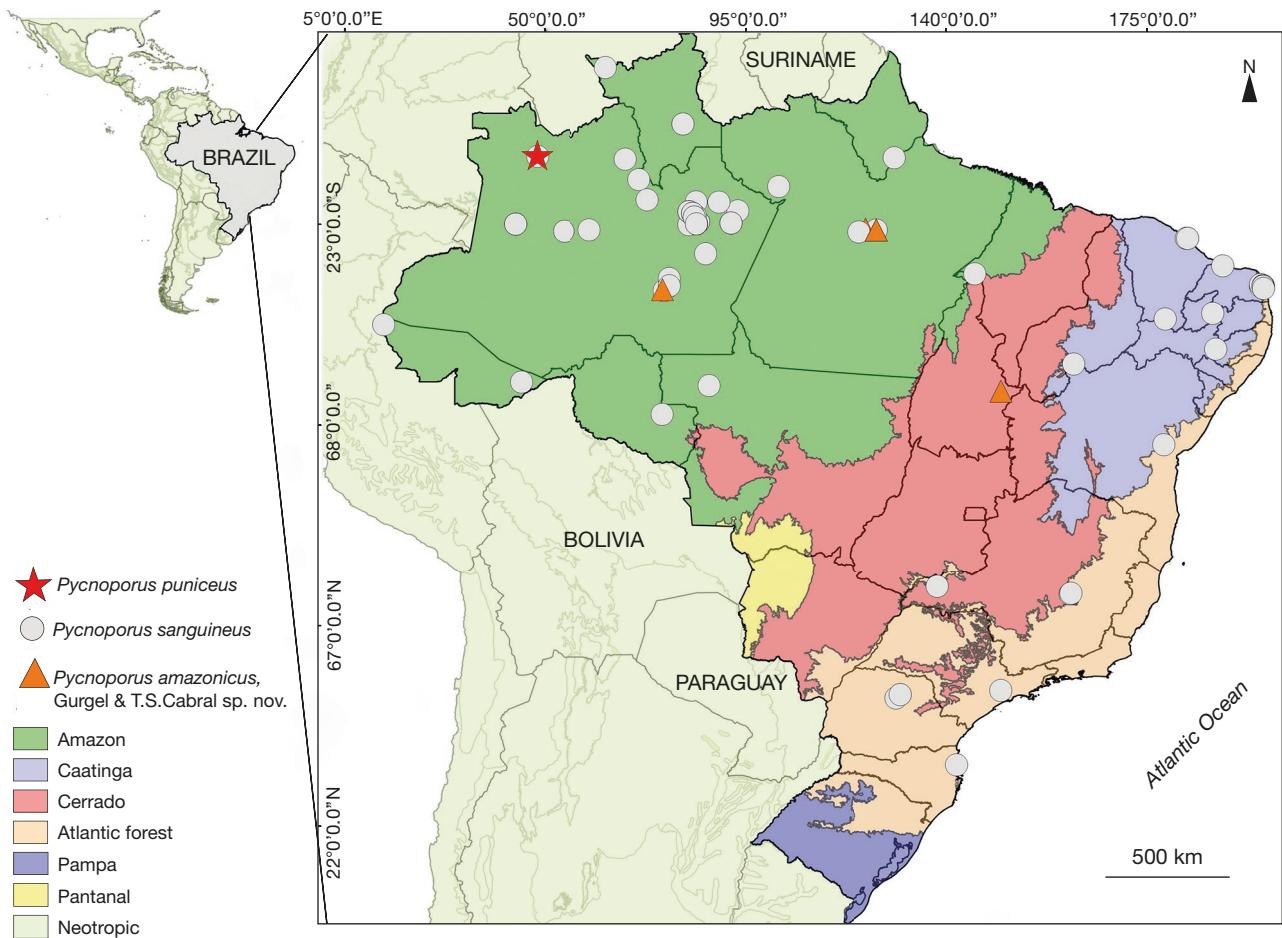


FIG. 1. — Map with the geographic distribution of the *Pycnoporus* P.Karst. from Brazil specimens analyzed in this study. Map created in the [Qgis.org](https://qgis.org) software.

Pycnoporus specimens from Brazil have been studied regarding their morphological, biochemical and ecological aspects (e.g., Silva 2010; Teixeira *et al.* 2018; Lima 2020; Figueredo *et al.* 2020; Leonardo-Silva *et al.* 2020), but they lack more robust taxonomic analyses that seek to understand the diversity of species in the genus that exists in the country.

Of the species of *Pycnoporus*, *P. sanguineus* has the widest distribution, since it exceeds transoceanic barriers and is reported for tropical and subtropical regions (Nobles & Frew 1962; Ryvarden & Johansen 1980). It was first described by Carl von Linné (1763) under *Boletus sanguineus* L. based on collections from Suriname. It is the only Neotropical polypore with an intense reddish-orange basidiome and a trimitic hyphal system, and is thus among the easiest to recognize (Ryvarden 2016). Although its coloration is a diagnostic character in well-preserved specimens, the species seems to demonstrate variations (for example, size, shape, color, and texture) depending on the substrate, environmental conditions, and the age of the basidiomata (Gilbertson & Ryvarden 1987; Téllez-Téllez *et al.* 2016), which can make identification difficult.

Several studies of macrofungi have shown that specimens with phenotypic plasticity and wide distribution, such as *P. sanguineus*, can mask the existing diversity within the genus, and the use of integrative taxonomy is an important tool that

can be used to understand such diversity (e.g., Costa-Rezende *et al.* 2016; Sousa *et al.* 2017; Accioly *et al.* 2019; Cabral *et al.* 2019; Oliveira *et al.* 2022). Therefore, we performed an analysis of *Pycnoporus* specimens collected in Brazil, with the integration of morphological and molecular data, and propose the description of a new species for science, two new records, a comparative table with the other species of the genus, and an identification key for the country. Lastly, we present the divergence time of the genus and its species, as a starting point for understanding the current diversification that exists in the genus.

MATERIAL AND METHODS

MORPHOLOGICAL ANALYSES

Morphological analyses were performed using dried specimens that were subsequently hydrated with 5% KOH. The specimens were collected between 2019 and 2022 in different Brazilian biomes, and from exsiccates of the UFRN-Fungi Herbarium, URM and INPA (Fig. 1) (acronyms according to Thiers [2024]). All specimens collected were deposited at Herbarium INPA-Fungos and this study is under SisGen AF6CC74.

Macroscopic analyses were performed via direct observations and with the aid of stereoscopic microscopes (Nikon SMZ1500 with a Nikon DS-Ri1 camera attached and Leica M205C). Macroscopic characteristics of the types (Gurgel *et al.* 2023) were analyzed using the ImageJ program (Schneider *et al.* 2012). The measurements of the macrostructures of the specimens were performed using the stereoscopic microscope software and a caliper, and included height (Min.) - height (Max.) × width (Min.) - width (Max.) mm or diameter (Min.) - diameter (Max.). A drop of 3% KOH was poured over the basidiomata to observe any possible coloration change. All colors observed here were determined following the Küppers color guide (Küppers 2002).

Slides were prepared with Melzer reagent to observe a dextrinoid (IKI+) or amyloid (IKI-) reaction, with cotton blue indicating a positive (CB+) or negative (CB-) cyanophilic reaction and, for better visualization of the hyaline structures, 1% Congo red dye was used (Ryvarden 2004). Then, the slides were observed under optical microscopes (Nikon Eclipse Ni (LM) with Nikon DS-Ri1 camera attached and Leica DM2500 LED). Whenever possible, 30 measurements were performed for basidiospores and 20 for other microstructures. All the measurements were performed in a KOH 5% solution. The statistical data calculations were performed in Excel, and included the mean length and width of basidiospores ($\bar{x}$ = mean) and the value of Qm, where Q is determined by dividing the value of length/width, and Qm is the mean of the values of Q. According to Bas (1969), the values represent the shape of the spores, where Q = 1.00-1.05 globose shape; Q = 1.05-1.15 subglobose; Q = 1.15-1.30 slightly ellipsoid; Q = 1.30-1.60 ellipsoid; Q = 1.60-2.00 elongated; Q = 2.00-3.00 cylindrical and Q > 3.00 bacilliform. The other microstructures are represented as follows: height (Min.) - height (Max.) × width (Min.) - width (Max.). In addition, scanning electron microscopy (SEM) was performed to observe the hyphae.

PHYLOGENETIC ANALYSES

The DNA extraction from dried material, amplification and sequencing protocols of the DNA regions were performed according to Cabral (2024). Three regions were amplified, ITS (ITS 1 + 5.8S + ITS2), LSU (partial region of the 28S) and the elongation factor 1 alpha (*tef1*), with the PCR conditions in accordance with Justo & Hibbett (2011) and Cabral (2024), using the primers ITS1-ITS4, LROR-LR5 and EF1-983F/EF1-1567R. For the purification of the PCR fragments, the ExoSAP-IT™ enzyme kit was used, according to the manufacturer's protocol. PCR fragment sequencing was performed using the Applied Biosystems Abi PRISM® BigDye™ Terminator Cycle Sequencing Ready Reaction kit v. 3.1, and precipitation was performed with a glycogen (20 mg/mL) and 3 M sodium acetate solution (NG solution). The primers used for sequencing were the same as the ones used for amplification.

Consensus sequences were obtained and edited in the Geneious R9 program (Kearse *et al.* 2012). The consensus obtained were subjected to a similarity search using the BLAST tool

(Basic Local Alignment Search Tool) in GenBank in order to verify possible contamination and whether the sequences generated corresponded to the desired regions. Sequences of ITS, LSU and *tef1* related to *Pycnoporus* or synonyms were obtained from GenBank for phylogenetic analysis.

The alignment of the sequences obtained in this study and sequences from GenBank were performed using MAFFT software, using advanced E-INS-i configurations (Katoh & Standley 2013), in order to identify homologous positions. Then, the alignment was manually edited in the AliView program (Larsson 2014). The software Mesquite v. 1.04 was used to construct the matrix of concatenated data (Maddison & Maddison 2006). Three phylogenetic analyses were performed: a first analysis with concatenated array of 5.8S, LSU, *rpb2* (second largest subunit of RNA polymerase II) and *tef1* to assess the position of the genus in the order Polyporales (dataset A). The *rpb2* data were obtained exclusively from GenBank; a second with a concatenated array of ITS, LSU and *tef1* using the species within the genus (dataset B); and a third with the alignment of ITS only with the species of *Pycnoporus*, which allows a greater sampling of sequences from different geographical regions (dataset C).

The best molecular evolution model for each group of markers was obtained through the jModelTest program (Guindon & Gascuel 2003; Darriba *et al.* 2012). Subsequently, Bayesian (BY) analyses were performed using MrBayes v. 3.1.2 (Ronquist & Huelsenbeck 2003) on the Cipres Science Gateway (<http://www.phylo.org/>) for 10 million generations for the datasets A and C and 5 million for dataset B; in two independent runs with four simultaneous chains, and trees sampled every 1 000 generations, using a relative burn-in of 0.25. A node was considered strongly supported if it had a Bayesian Posterior Probability (PP) of ≥ 0.95. However, for the tree of ITS and the concatenated matrix of relationship between species in the genus, the most divergent grouping within the clade was used as the root, this being the clade of *P. puniceus* (Fr.) Ryvarden. For the genus relationship tree in Polyporales, *Thelephora ganbajun* M. Zang and *Tomentella* sp. were used as external groups, according to Zhao *et al.* (2017).

In view of the absence of type material DNA sequences, we used reference sequences designated according to Lesage-Meessen *et al.* (2011), according to the proximity of the type location, these being specimen CIRM-BRFM 902 from Suriname designated as reference for *P. sanguineus*; MUCL 38523 from Australia for *P. coccineus* (Fr.) Bondartsev & Singer, and MUCL 30555 from Belgium for *P. cinnabarinus* (Jacq.) P.Karst. We also used BCC 26408 from Thailand as a reference for *P. puniceus* due to its proximity to the type locality (Malaysia). The resulting trees were edited in FigTree (<http://tree.bio.ed.ac.uk/software/figtree/>).

MOLECULAR DATING ANALYSIS

The sequences of the concatenated genes (dataset A) were subjected to a divergence time analysis via molecular dating using a Bayesian approach as an initial step in order to

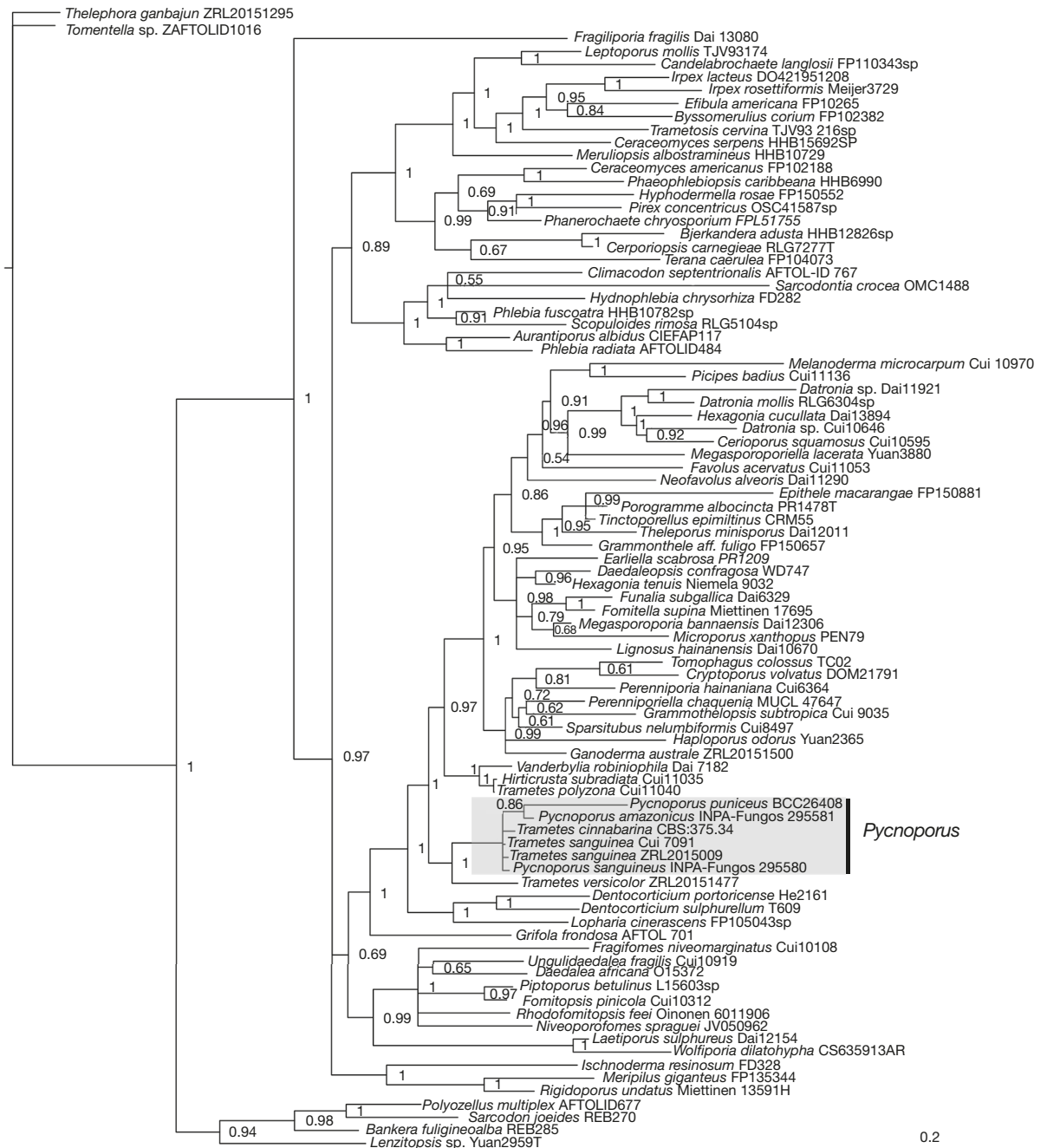


FIG. 2. — Bayesian inference phylogenetic tree of *Pycnoporus* P.Karst. and other genera in Polyporales using 5.8S, LSU, *rpb2* and *tef1* concatenated data. Posterior Probability (PP) values for each node are shown.

understand the evolutionary history of the genus. The analysis was performed in the BEAST v. 1.8.0 program (Drummond & Rambaut 2007), and the BEAST input files were built using BEAUti. The substitution models were chosen separately for each partition based on previous inference by the jModelTest (Darriba *et al.* 2012), as previously described. Representatives of *Meripilus giganteus* (Pers.) P.Karst., *Rigidoporus undatus* (Pers.) Donk, and *Ischnoderma resinosum* (Schrad.) P.Karst. were used as an external group, according to the dataset available by Zhao *et al.* (2017).

Two primary calibration points were included in our analyses following the information contained in Zhao *et al.* (2017) and He *et al.* (2019) since fossil record data are limited: mean root ages in Polyporales (183 Mya) and of the families (Fomitopsidaceae Jülich 88 Mya, Irpicaceae Spirin & Zmitr. 62 Mya, Meruliaceae P.Karst. 81 Mya, Meripilaceae Jülich 106 Mya, Phanerochaetaceae Jülich 62 Mya, Polyporaceae Fr. ex Corda 88 Mya). Uncorrelated lognormal relaxed-clock analysis was used, specifying ulcd.mean as the prior parameter for the gamma distribution (scale = 0.001, shape = 1), to estimate the

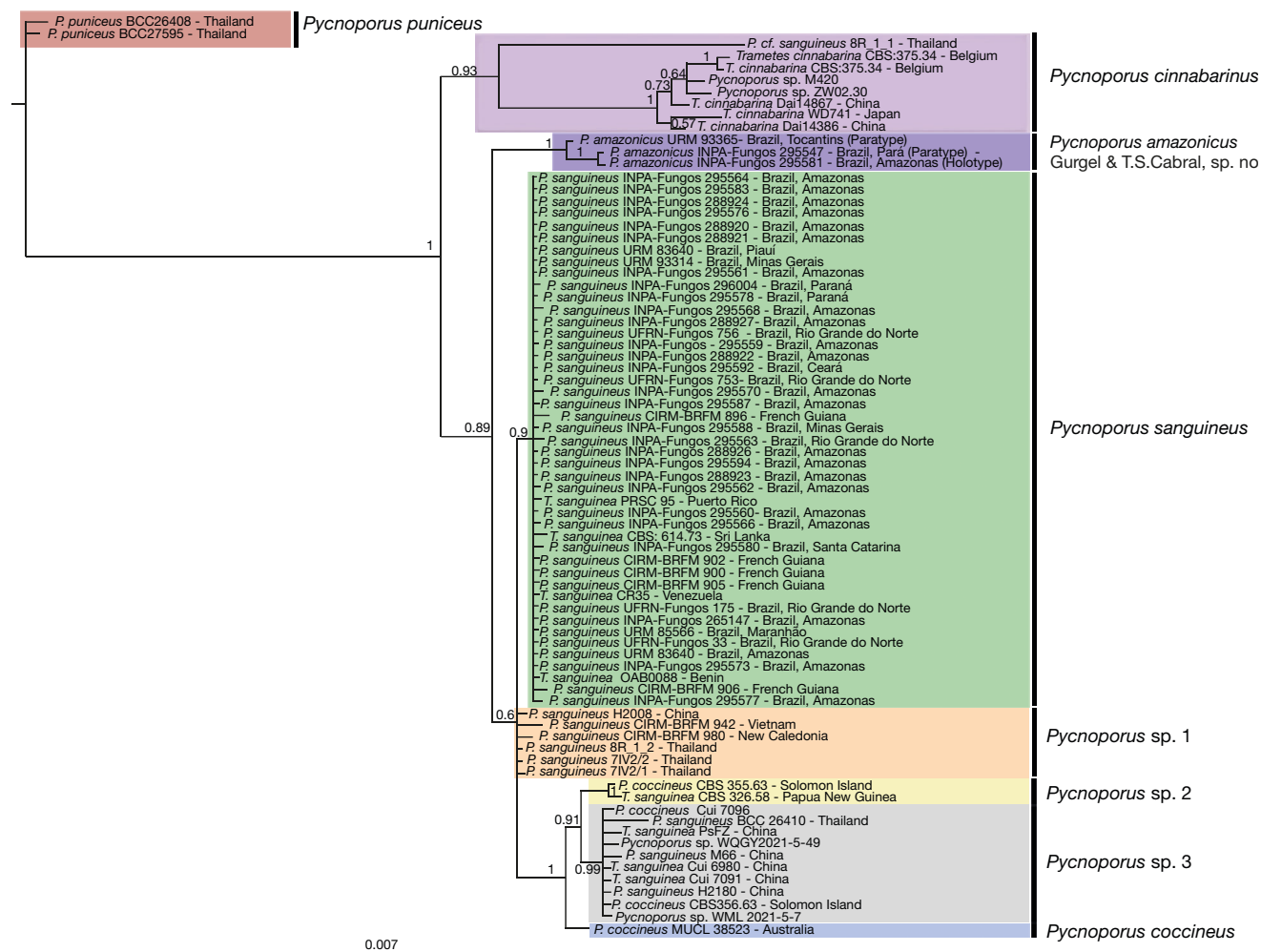


FIG. 3. — Phylogenetic reconstruction of ITS, LSU and *tef1* concatenated data positioning *Pycnoporus amazonicus* Gurgel & T.S.Cabral, sp. nov. within the genus *Pycnoporus* P.Karst., constructed from Bayesian Inferences with Posterior Probability (PP) values at the nodes.

divergence time and the respective credibility intervals. The posterior distributions of the parameters were obtained using MCMC analysis for 100 million generations, with a burn-in percentage of 25%. Samples of the posterior distributions were summarized into a maximum clade credibility tree with the maximum sum of posterior probabilities listed on their internal nodes using TreeAnnotator v1.8.0 (Drummond & Rambaut 2007). The posterior convergence was evaluated using the Tracer v. 1.4 software, concatenating the runs in a final tree with the ages of the nodes estimated as the mean of the highest density value after 95% (HPD). FigTree was used to visualize the resulting tree and obtain the means.

RESULTS

A total of 103 exsiccates were analyzed, 37 coming from herbaria and 66 recently collected. Of these, 72 are distributed in the Brazilian Amazon, 17 in the Atlantic Forest, 10 in the Caatinga and four in the Cerrado biomes, representing three species. We obtained 104 sequences including 42 ITS, 34 from LSU and

28 from *tef1* (Table 1). The final alignment of the matrix corresponding to Polyporales (dataset A) contained 2 298 positions (174 for 5.8S, 942 for LSU, 748 for *rpb2* and 434 for *tef1*); the concatenated matrix (dataset B) contained 2000 pb (643 for ITS, 871 for LSU, 486 for *tef1*) and 77 taxa; and the matrix of ITS (dataset C) contained 624 pb and 198 taxa. The evolutionary models selected for each dataset were as follows: for dataset A, HKY+I+G (5.8S) and GTR+I+G (LSU, *tef1*, and *rpb2*) were chosen; for dataset B, GTR+I+G (ITS) and GTR+G (LSU and *tef1*) were chosen; for dataset C, SYM (ITS) was chosen. The sequences generated in this study are listed in Table 1, and the sequences downloaded from Genbank are presented in Appendix 1.

In 5.8S, LSU, *rpb2* and *tef1* dataset (Fig. 2), *Pycnoporus* forms a monophyletic group within the order Polyporales, with *Trametes versicolor* (L.) Lloyd as its sister group, well supported (PP = 1). Four species grouped in the *Pycnoporus* clade, *P. puniceus*, *P. sp. nov.* (see taxonomy), *P. cinnabarinus* (synonym of *Trametes cinnabarina*) and *P. sanguineus* (synonym of *Trametes sanguinea*). *Pycnoporus amazonicus* Gurgel & T.S.Cabral, sp. nov. appears as a sister group of *P. puniceus*, but with low support (PP = 0.85).

TABLE 1. — Specimens of *Pycnoporus* P.Karst. included in molecular analyses obtained in this study and the Genbank access number for each sequence region.

Taxa	Voucher	Country	ITS	LSU	<i>tef1</i>
<i>Pycnoporus amazonicus</i> Gurgel & T.S.Cabral, sp. nov.	INPA-Fungos 295581 - Holotype	Brazil	OP198494	OP198567	PP988043
—	INPA-Fungos 295547	Brazil	OP198492	OP198565	—
—	URM 93365	Brazil	OP198493	OP198566	—
<i>Pycnoporus puniceus</i> (Fr.) Ryvarden	INPA-Fungos 297904	Brazil	PP198347	—	—
<i>Pycnoporus sanguineus</i> (L.: Fr.) Murrill	UFRN-Fungos 756	Brazil	OP198470	—	PP988033
	UFRN-Fungos 753	Brazil	OP198474	OP198535	—
	UFRN-Fungos 175	Brazil	OP198486	OP198561	PP988026
	UFRN-Fungos 33	Brazil	OP198489	OP198562	PP988018
	URM 83640	Brazil	OP198463	OP198538	PP988035
	URM 93314	Brazil	OP198464	OP198537	—
	URM 85566	Brazil	OP198488	OP198548	—
	INPA-Fungos 295586	Brazil	OP723293	—	—
	INPA-Fungos 295587	Brazil	OP198476	OP198556	PP988023
	INPA-Fungos 295588	Brazil	OP198477	OP198539	PP988037
	INPA-Fungos 295559	Brazil	OP198471	—	PP988034
	INPA-Fungos 295560	Brazil	OP198483	OP198549	PP988040
	INPA-Fungos 295590	Brazil	OP723292	—	—
	INPA-Fungos 295592	Brazil	OP198473	OP198557	—
	INPA-Fungos 295580	Brazil	OP198485	OP198558	PP988015
	INPA-Fungos 295594	Brazil	OP198480	—	PP988028
	INPA-Fungos 295561	Brazil	OP198465	OP198559	PP988025
	INPA-Fungos 295576	Brazil	OP198460	OP198547	—
	INPA-Fungos 295562	Brazil	OP198482	OP198560	PP988041
	INPA-Fungos 295563	Brazil	OP198478	OP198540	PP988024
	INPA-Fungos 295564	Brazil	OP198457	OP198550	PP988022
	INPA-Fungos 295577	Brazil	—	OP198541	PP988019
	INPA-Fungos 295583	Brazil	OP198458	OP198551	PP988014
	INPA-Fungos 288927	Brazil	OP198469	OP198552	PP988039
	INPA-Fungos 288923	Brazil	OP198481	OP198542	PP988042
	INPA-Fungos 288926	Brazil	OP198479	OP198534	—
	INPA-Fungos 288924	Brazil	OP198459	OP198543	PP988029
	INPA-Fungos 288922	Brazil	OP198472	—	PP988021
	INPA-Fungos 288920	Brazil	OP198461	OP198553	PP988031
	INPA -Fungos 288921	Brazil	OP198462	OP198554	PP988032
	INPA-Fungos 296004	Brazil	OP198466	OP198536	PP988027
	INPA-Fungos 265147	Brazil	OP198487	OP198564	—
	INPA-Fungos 295578	Brazil	OP198467	OP198544	PP988036
	INPA-Fungos 295566	Brazil	OP198484	OP198545	PP988017
	INPA-Fungos 295567	Brazil	OP198490	OP198555	PP988030
	INPA-Fungos 295568	Brazil	OP198468	OP198546	PP988016
	INPA-Fungos 295570	Brazil	OP198475	—	PP988020
	INPA-Fungos 295572	Brazil	OP723291	—	—
	INPA-Fungos 295573	Brazil	OP198491	OP198563	PP988038

A combined (ITS, LSU and *tef1*) dataset of *Pycnoporus* (Fig. 3), recovered eighteen major clades. Five species were identified according to the position of the reference sequences, geographical data and/or morphological data (Lesage-Meessen *et al.* 2011, Téllez-Téllez *et al.* 2016): 1) *P. puniceus*, containing sequences from Thailand; 2) *P. cinnabarinus*, with support value PP = 0.93, grouping sequences from Thailand, Belgium, China and Japan; 3) *Pycnoporus amazonicus* Gurgel & T.S.Cabral, sp. nov., strongly supported, containing three sequences from Brazil from different localities, and which, together with the morphological data, proved to be a new species for science; 4) *P. sanguineus*, with low support (PP = 0.9), including species from Brazil, Puerto Rico, Sri Lanka, French Guiana, Venezuela and Benin; and 5) *P. coccineus*, with maximum support and containing sequences from Australia. The other three clades were identified as *Pycnoporus* sp.: 6) *Pycnoporus* sp. 1 with

low support and with localities for China, Vietnam, New Caledonia and Thailand; 7) *Pycnoporus* sp. 2 with maximum support, for Solomon Island and Papua New Guinea; and 8) *Pycnoporus* sp. 3, strongly supported (PP = 0.99), with sequences for Thailand, China and Solomon Island. In this dataset, *Pycnoporus* sp. appears as a sister group of the clade formed by *P. sanguineus*, *Pycnoporus* sp. 1, 2, 3, and *P. coccineus*, with low support (PP = 0.89).

The ITS matrix dataset for *Pycnoporus* (Fig. 4) returned seven clades and the general topology was similar to that of the combined data (ITS, LSU and *tef1*), but with higher support values and larger geographical representativeness. Five species were identified: *Pycnoporus* sp. (PP = 1, Brazil); *P. coccineus* (PP = 0.99, Austria and Australia); *P. sanguineus* (PP = 1, Argentina, Brazil, India, Philippines, Taiwan, China, Thailand, New Caledonia, Sri Lanka, Papua

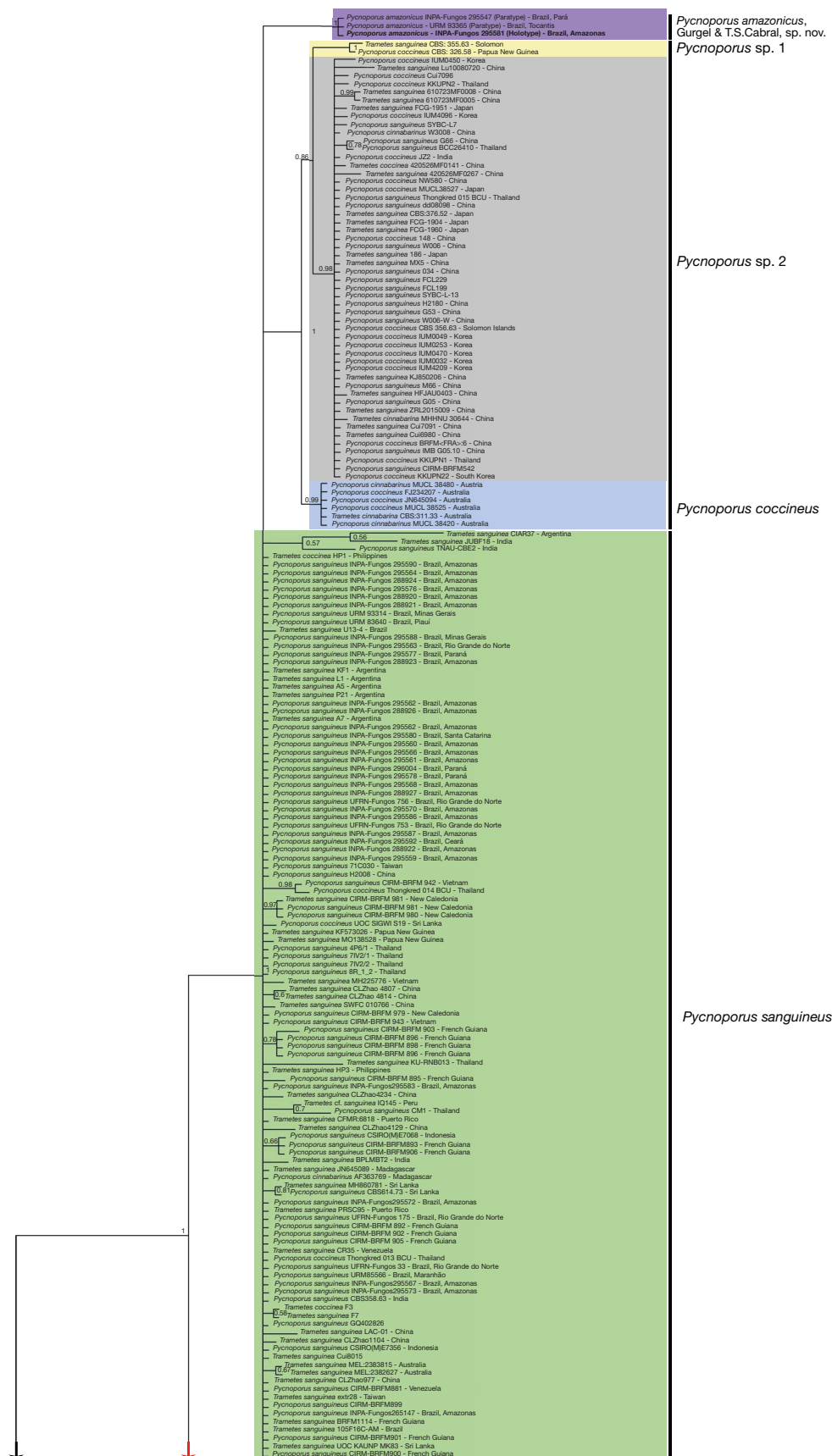


FIG. 4. — Bayesian inference phylogenetic tree of *Pycnoporus* P.Karst. species from the ITS dataset. Posterior Probability (PP) values for each node are shown.

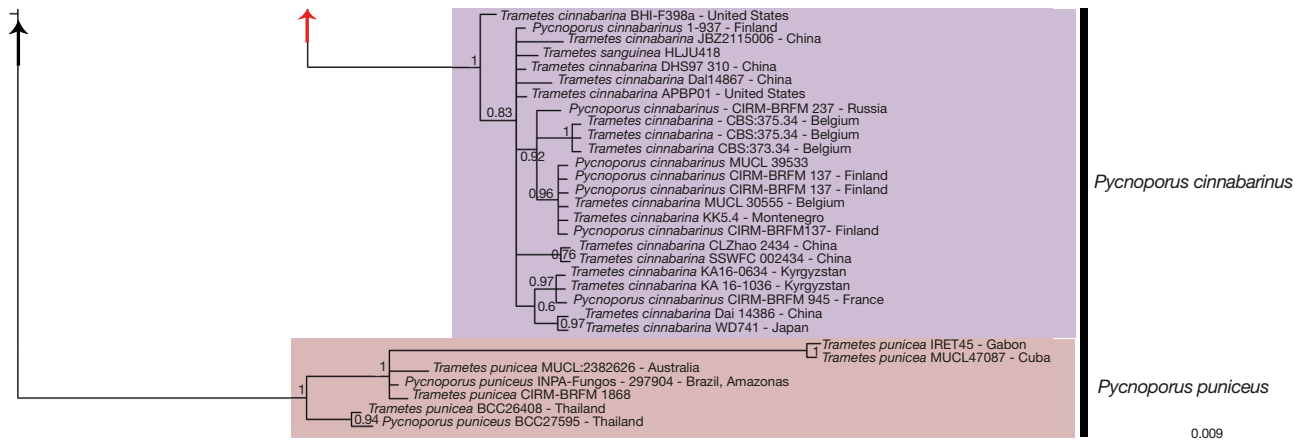


Fig. 4. — Continuation.

IDENTIFICATION KEY FOR *PYCNOPORUS* P.KARST. SPECIES OCCURRING IN BRAZIL

1. Basidiomata stipitate to substipitate, zonate, with pores 5-8 per mm, reddish orange to vivid orange..... *Pycnoporus sanguineus*
- 1' Basidiomata azonate, with pores 1-5 per mm 2
2. Basidiomata rigid, with pores 1-3 per mm, cinnabar red, context compactus, with cinnabar tones and without line..... *Pycnoporus puniceus*
- 2' Basidiomata soft, with pores 3-5 per mm, orange to matte orange, context with brown tones and with line between context and tubes *Pycnoporus amazonicus* Gurgel & T.S.Cabral, sp. nov.

New Guinea, Vietnam, French Guiana, Peru, Puerto Rico, Venezuela, Indonesia, Madagascar and Australia); *P. cinnabarinus* (PP = 1, United States, Finland, China, Russia, Belgium, France, Finland, Montenegro, Kyrgyzstan and Japan); and *P. puniceus* (PP = 1, Gabon, Cuba, Australia, Brazil and Thailand). In general, the internal relationships of the *P. sanguineus* clade receive little support. Two clades were identified as *Pycnoporus* sp.: *Pycnoporus* sp. 1 (PP = 1, Solomon Island and Papua New Guinea); *Pycnoporus* sp. 2 (PP = 0.86, Korea, China, Thailand, Japan, India and Solomon Island).

In both analyses (Figs 3; 4), the Brazilian specimens sampled grouped into three clades, corresponding to *P. puniceus*, *P. sanguineus* and *Pycnoporus* sp.

According to the molecular analysis with estimated divergence times (Fig. 5; Table 2), *Pycnoporus* and *Trametes* diverged during the Eocene at 36.9 Mya (19-59 Mya) and *Pycnoporus* diversified into two clades at 14.3 Mya (6-25 Mya) ago, and dates back to the Miocene. The clade of *P. puniceus* and *P. amazonicus* Gurgel & T.S.Cabral, sp. nov. was the first to diversify within *Pycnoporus*, 10.6 Mya (4-20 Mya) ago and, more recently, 5 Mya (1-10 Mya) ago there was diversification between *P. sanguineus* (Neotropical) and the clade with *P. cinnabarinus*, *Pycnoporus* sp. (as *Trametes sanguinea* voucher ZRL2015009, from China) and *Pycnoporus* sp. (as *Trametes sanguinea* voucher Cui 7091, Australia).

SYSTEMATICS

Family POLYPORACEAE Fr. ex Corda

Genus *Pycnoporus* P.Karst.*Revue de Mycologie*, 3 (9): 16-19 (Karsten 1881) nom. cons.*Xylometron* Paulet, *Prospectus du traité historique, graphique, culinaire, et médical des champignons*: 1-94 (Paulet 1808).TYPE SPECIES. — *Pycnoporus cinnabarinus* (Jacq.) P. Karst. (Karsten 1881). (synonym of *Boletus cinnabarinus* Jacq. (Jacquin 1776) and *Polyporus cinnabarinus* (Jacq.) Fries (Fries 1821), nom. sanct.).

DESCRIPTION

Annual basidiome, solitary to gregarious, sessile to effuse-reflex, dimidiolate to strongly attached, semicircular, coriaceous. Pileus smooth, bright reddish-orange to cinnabar red, sometimes paler, and majority with zones. Margin thickened becoming thin with time, Acute to obtuse, entire to irregular, concolor to the pileus. Context fibrous, thin to thick, sometimes with orange to pale orange zones, and may be brown and bluish, becoming black when in contact with 5% KOH, sometimes with a pale yellow to grayish brown between context and tubes. Pore surface with circular, angular to irregular pores, 3-8 per mm, concolor to the pileus; tubes with one or two layers. Stipe absent or in the form of a short, central stalk. Generative hyphae with clamps; skeletal with thick walls,

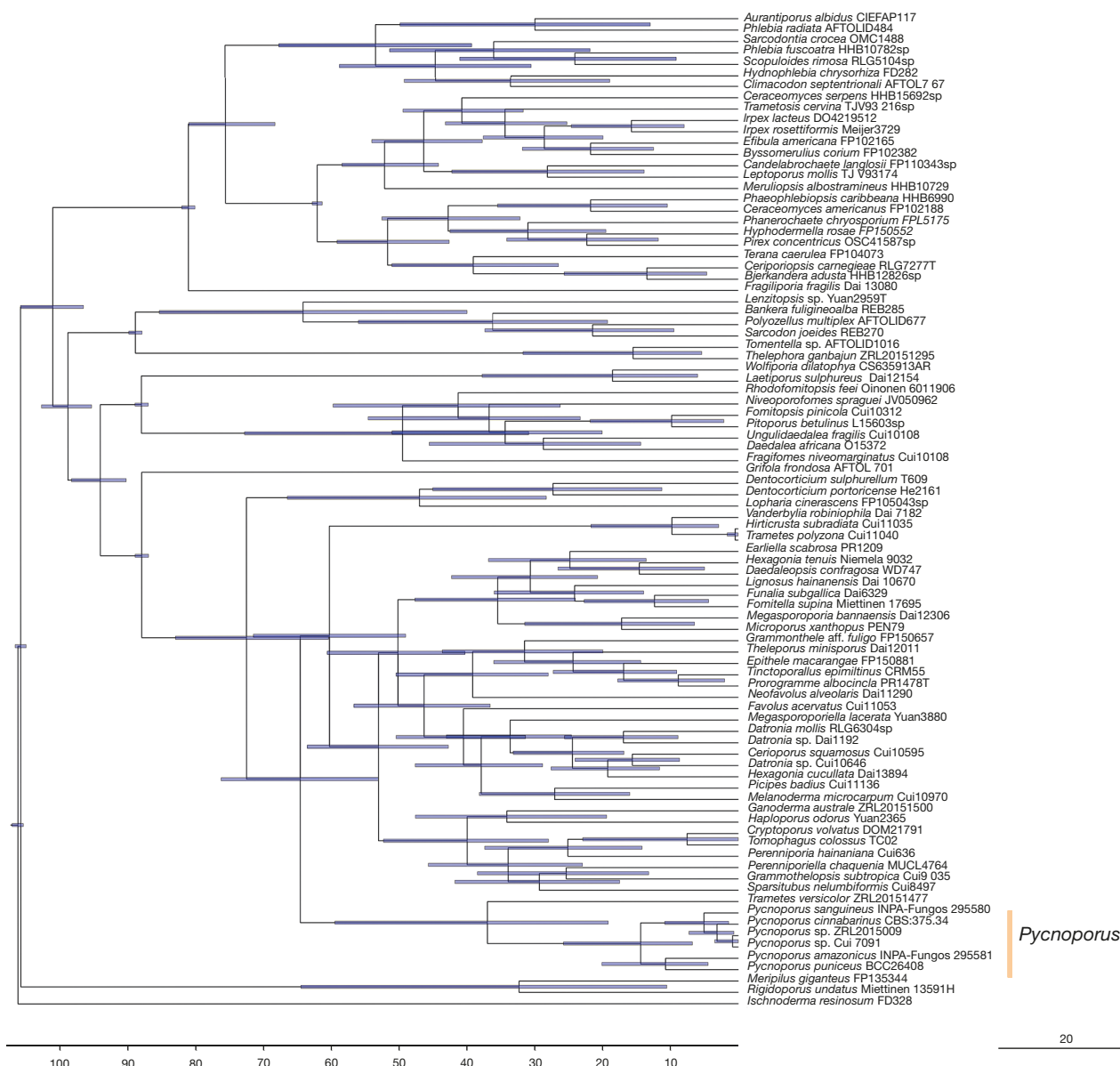


FIG. 5. — Phylogeny with divergence estimation in Polyporales, calculated by relaxed molecular clock through Bayesian inference of concatenated data matrix (ITS, LSU, *tef1*) in BEAST software, with calibration based on data provided by Zhao et al. (2017) and He et al. (2019). Horizontal bars indicate the 95% HPD values.

sometimes with orange crystals, dextrinoid, present throughout the basidiome; binding hyphae with short branches and thick and irregular walls, more numerous in the context than in the tubes. Clavate basidium, with four sterigmata. Elongated and slightly curved, smooth, hyaline basidiospores in 5% KOH, CB-; IKI-.

Pycnoporus amazonicus Gurgel & T.S.Cabral, sp. nov.
(Figs 6; 9A, D, G; 10A-D)

TYPE MATERIAL. — **Brazil** • Amazonas, Manicoré, Comunidade Barro Alto; 05.VII.2021; D.L. Komura leg.; *DLK3268100*; holotype: INPA-Fungos 295581; GenBank: *OP198494*-ITS, *OP198567*-

LSU, *PP988043-tef1* • Pará, Altamira, Trans Assurini, Travessão da firma; 3°16'47"S, 52°34'54"W; 17.VII.2021; R.J.S. Dalman leg.; *RJS51119*; paratype: INPA-Fungos 295548 • same data; 09.VII.2022; R.J.S. Dalman leg.; *RJS225128*; paratype: INPA-Fungos 295551 • same data; 14.VIII.2022; R.J.S. Dalman leg.; *RJS252130*; paratype: INPA-Fungos 295552 • same data; R.J.S. Dalman leg.; *RJS253131*; paratype: INPA-Fungos 295553 • same data; R.J.S. Dalman leg.; *RJS254132*; paratype: INPA-Fungos 295554 • same data; R.J.S. Dalman leg.; *RJS255133*; paratype: INPA-Fungos 295555 • same data; R.J.S. Dalman leg.; *RJS256134*; paratype: INPA-Fungos 295556 • Novo, Vicinal da 16; 10.VII.2021; R.J.S. Dalman leg.; *RJS27118*; paratype: INPA-Fungos 295547 • same data; 27.VII.2022; R.J.S. Dalman leg.; *RJS224125*; paratype: INPA-Fungos 295550 • Tocantins, Mateiros, Parque Estadual do Jalapão; 24.VI.2018; T.B. Gilbertoni leg.; *TBG15*; paratype: URM 93365.

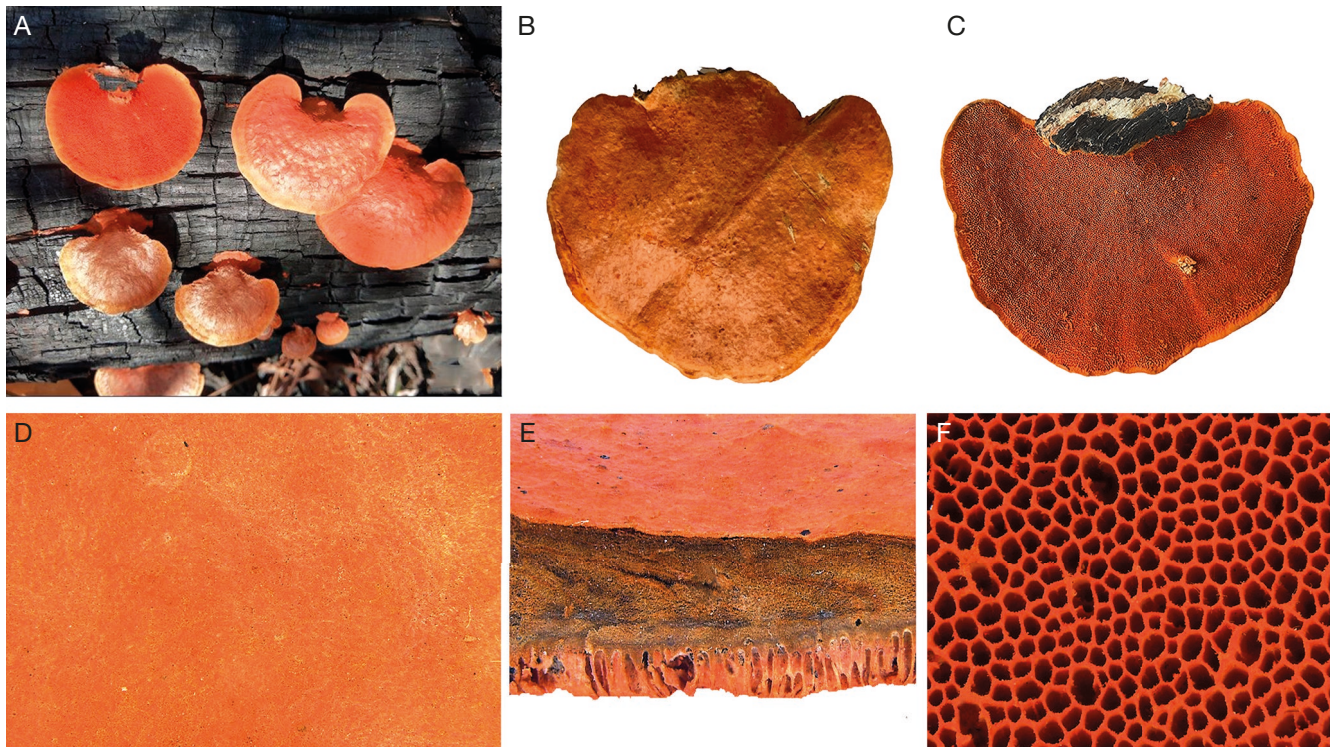


FIG. 6. — Macroscopic view of *Pycnoporus amazonicus* Gurgel & T.S.Cabral, sp. nov.: **A**, basidiomata in the field; **B**, **C**, basidiomata dried basidiomata; **D**, details of the pileus; **E**, details of the context and tubes; **F**, hymenophore. **A**, **D**–**F**, holotype (INPA-Fungi 295581); **B**, **C**, paratype (INPA-Fungi 295553). Scale bars: **A**, 20 mm; **B**, **C**, 10 mm; **D**, **E**, 2 mm; **F**, 1 mm.

TABLE 2. — Estimated divergence times obtained in molecular analyses.

	Mean age (Mya)	95% Height posterior density (Mya)
<i>Pycnoporus</i> P.Karst.	14.35	6.74–25.7
<i>Pycnoporus amazonicus</i> Gurgel & T.S.Cabral, sp. nov. & <i>P. puniceus</i> (Fr.) Ryvarden	10	4.45–20.05
<i>P. sanguineus</i> (Fr.) Ryvarden	5.03	1.42–0.8
<i>P. cinnabarinus</i> (Jacq.) P.Karst.	3.11	0.63–7.24
<i>Pycnoporus</i> sp. (as <i>Trametes sanguinea</i> voucher ZRL2015009) & <i>Pycnoporus</i> sp. (as <i>Trametes sanguinea</i> voucher Cui 7091)	0.82	0–3.44

DIAGNOSIS. — Differs from the other species in the genus by the basidiome with a soft aspect, orange to matt orange, with brown context mixed with orange and cream zones barely visible, gray line between context and hymenophore, 3–5 pores per mm, with smooth, elongated basidiospores, $5.7\text{--}7.9 \times 3.0\text{--}4.8\ \mu\text{m}$. It is distinguished from *P. coccineus* by its context with predominating pale orange zones with moderate orange-yellow, and smaller spore sizes $4.0\text{--}5.2 \times 2.0\text{--}2.3$, and from *P. sanguineus* by its 5–8 pores per mm in the hymenophore.

ETYMOLOGY. — In reference to Amazonia, where the holotype was collected.

DISTRIBUTION. — So far known for Brazil in the Brazilian Amazon (Amazonas and Pará) and the Cerrado biome (Tocantins).

SUBSTRATE. — Growing on burnt dead trunk of an indeterminate angiosperm and causing white rot.

MYCOBANK. — MB850045.

DESCRIPTION

Basidiome perennial, gregarious, cespitose; varying in shape from dimidiate, dimidiate elongated, semicircular, with attack on the substrate ranging from strongly adhered to semistipitate, 67–115 mm diameter $\times$ 47–66 mm width $\times$ 4–5 mm thickness, soft and malleable when young, coriaceous with age. Pileus surface crusty to smooth, velvety to tomentose, bluish, slightly glossy to opaque, orange ($N_{00}Y_{90}M_{60}$) to matt orange ($N_{00}Y_{99}M_{60}$), and the whole surface becomes yellowish white ($N_{00}Y_{20}M_{00}$) at high temperatures and in older specimens. Margin thick, acute to obtuse, entire to irregular, concolor to pileus surface, or pale orange ($N_{00}Y_{80}M_{50}$). Context and pileus surface form distinct layers in cross-section, fibrous and soft-compact, 2–3 mm thick, non-homogeneous zones, predominantly brown ($N_{60}Y_{99}M_{70}$), sometimes merged with orange ($N_{00}Y_{90}M_{60}$) and cream ($N_{00}Y_{40}M_{10}$) zones, with homogeneous orange ($N_{00}Y_{90}M_{60}$) and cream ($N_{00}Y_{40}M_{10}$) zones in

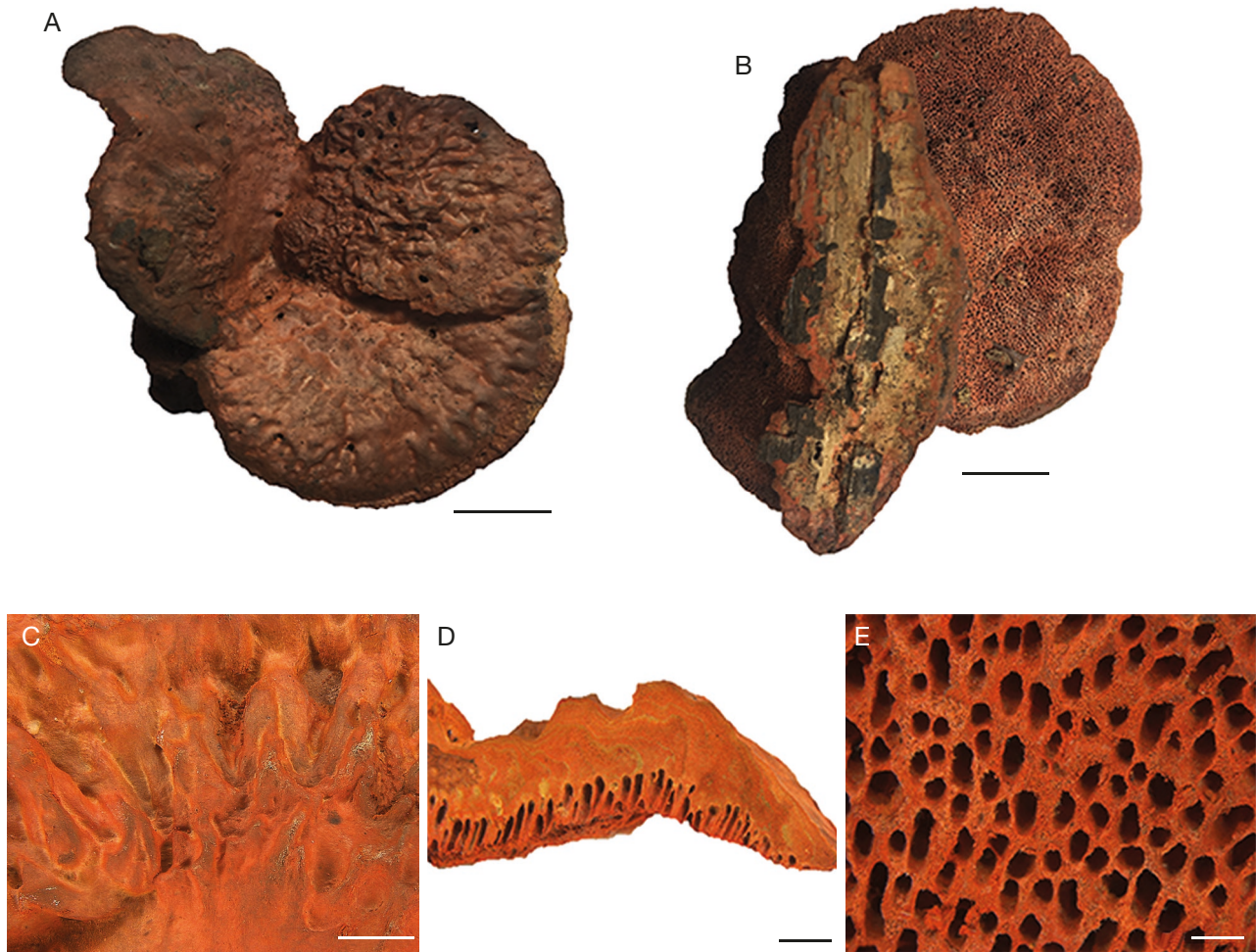


FIG. 7. — Macroscopic view of *Pycnoporus puniceus* (Fr.) Ryvarden (INPA-Fungi 297904): **A, B**, general view of the basidiome; **C**, details of the pileus; **D**, details of the context and tubes; **E**, hymenophore. Scale bars: A, B, 20 mm; C, D, 2 mm; E, 1 mm.

the apical portion, reflecting the developmental stage. Line grayish brown ($N_{60}C_{00}M_{10}$) and cream ($N_{00}Y_{40}M_{10}$), between the context and the hymenophore. Surface of the pores of the hymenophore bright orange ($N_{00}C_{90}M_{60}$) to moderate reddish orange ($N_{00}C_{90}M_{80}$); pores circular, angular to irregular, 3-5 pores per mm, 0.2×0.3 mm diameter; dissepiment thin, entire or lacerated, concolor to the pore surface; tube circular with 1 layer up to 2-2.5 mm deep, about 0.4 mm wide, light orange ($N_{00}C_{80}M_{50}$). Macrochemical reaction occurs when adding 5% KOH resulting in a rapid color change from black to greenish brown in part of the basidiome. Hyphal system trimitic. Pileus surface composed of generative hyphae, 2-4 μ m diameter, thin-walled to slightly thick, fused to abundant skeletal hyphae, 3-4 μ m diameter, hyaline in 5% KOH, CB-; IKI-. Context composed of generative hyphae thin-walled, with frequent clamps, rarely branched, 2-4 μ m diameter, hyaline to yellowish in 5% KOH, CB-; IKI-; skeletal hyphae dominate, thick-walled, non-septate, unbranched, straight or slightly tortuous, 3-7 μ m diameter, hyaline to yellowish in 5% KOH, CB-; IKI-; binding hyphae thick-walled, non-septate, branched with short branches, 2-4 μ m diameter, hyaline to yellowish in 5% KOH, CB-; IKI-. Trama of the tubes composed of hyphae

similar to the context; skeletal hyphae, 2-5 μ m diameter; connective binding hyphae more conspicuous than context, 1-3 μ m diameter. Hyphae with orange crystals predominate in all the parts of the basidiome, 2-4 μ m diameter, hyaline in 5% KOH, CB-; IKI-. Basidium clavate, 10-16 $\times$ 5-7 μ m, with basal clamp, four sterigmata, hyaline in 5% KOH, CB-; IKI-. Basidiospores $5.72-7.96 \times 3.06-4.83$ μ m ($x = 6.92 \pm 0.6 \times 4.01 \pm 0.5$; $Qm = 1.7$), elongated, smooth, slightly curved, hyaline in 5% KOH, CB-; IKI-.

REMARKS

There is little clarity on the taxonomic value of some morphological characters, such as the presence of a line between context and hymenophore observed in *Pycnoporus amazonicus* Gurgel & T.S.Cabral, sp. nov. This characteristic is observed below the pileipellis, sometimes in *Trametes betulina* (L.) Pilát, *T. hirsuta* (Wulfen) Lloyd, and *T. versicolor* (L.) Lloyd, and always in the clade *meyenii* (Welti *et al.* 2012). On the other hand, the absence of a black line below the pileus, allied to a glabrous upper surface, and the absence of parietal crystals were diagnostic characteristics used to recognize *Leiotrametes* Welti & Courtec. (synonym of *Cubamyces* Murrill) (Justo & Hibbett 2011; Welti *et al.* 2012).

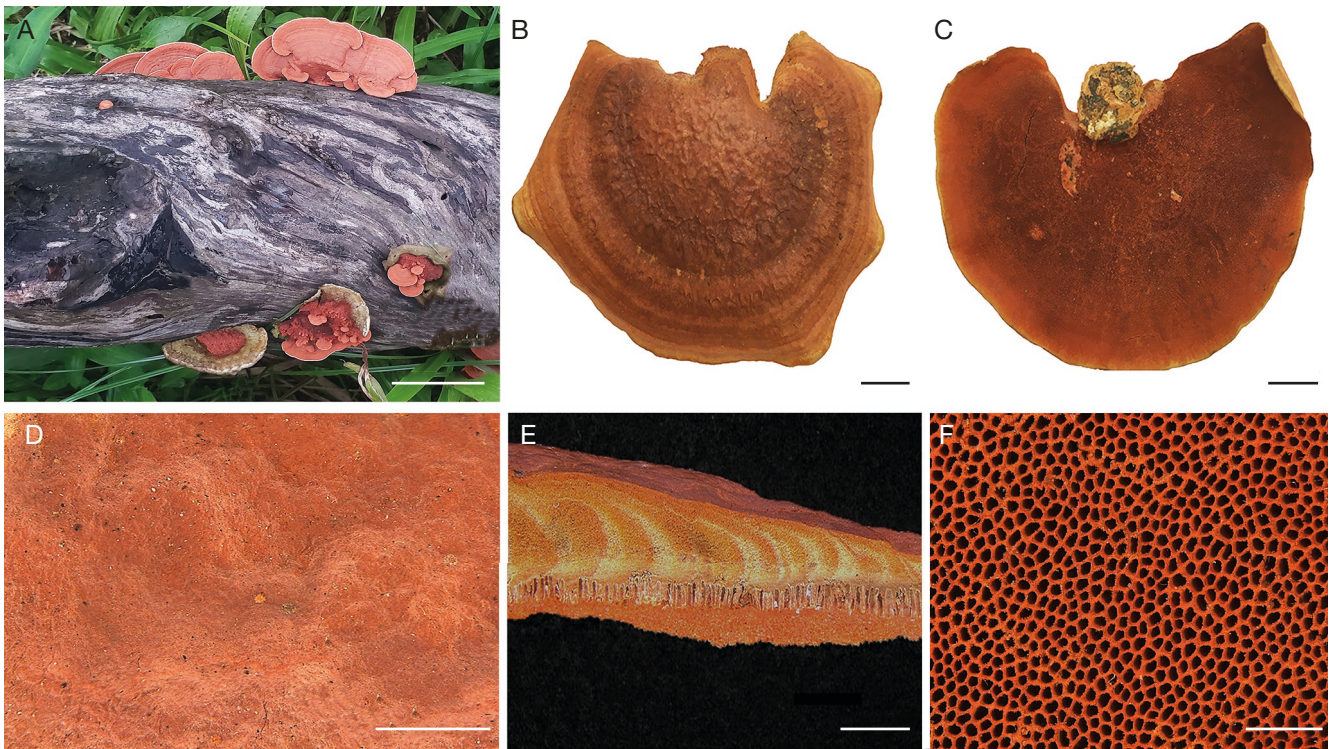


FIG. 8. — Macroscopic view of *Pycnoporus sanguineus* (L.: Fr.) Murrill: **A**, basidiomata in the field (INPA- Fungi 298920); **B**, **C**, basidiomata after dehydration (URM 93314); **D**, details of the pileus (INPA-Fungi 295549); **E**, details of the context and tubes (INPA-Fungi 295549); **F**, hymenophore (INPA-Fungi 295583). Scale bars: A, 30 mm; B, C, 10 mm; D, E, 2 mm; F, 1 mm.

For the species within *Pycnoporus*, this characteristic was shown to be delimitative, and we report the presence of this characteristic for the first time in specimens of the genus.

When compared to other species in the genus, *P. sanguineus* has a smooth, zoned pileus, 5–8 pores per mm, context with alternating white and medium orange, scaly to cottony zones, and *P. coccineus* has a smooth pileus, pores 3–5 per mm, and a context of a pale color, with predominant zones alternating from white to moderate orange (Nobles & Frew 1962, lectotype analysis), while *P. amazonicus* Gurgel & T.S.Cabral, sp. nov. has a smooth to tomentose pileus, 3–5 pores per mm, and a context sometimes not visible, predominantly brown, with a grayish line between the context and the hymenophore. With respect to the other two species of the genus, *P. cinnabarinus* has a thicker basidiome (170 mm), 1–4 circular pores per mm (Nobles & Frew 1962, lectotype analysis), and *P. puniceus* has a well-supported morphology and phylogeny, with a cinnabar pileus, 1–3 irregular pores per mm and a context with intense and lighter cinnabar zones (Nobles & Frew 1962; Ryvarden & Johansen 1980; lectotype analysis).

Thus, the morphological characteristics of colours and appearance of the context allied to the presence of a line between the context and the hymenophore and the numbers of pores per mm present in the hymenophore, together with the phylogenetic position within *Pycnoporus*, forming strongly supported clades in two of the phylogenies (Figs 3; 4), provide evidence that *Pycnoporus amazonicus* Gurgel & T.S.Cabral, sp. nov. is a distinct species.

Pycnoporus puniceus (Fr.) Ryvarden
(Figs 7; 9B, E, H; 10E–H).

Norwegian Journal of Botany, 19: 229–238. (Ryvarden 1972). — *Trametes punicea* Fries, *Nova Acta Regiae Societatis Scientiarum Upsaliensis* 3 (1): 17–136. (Fries 1851 [1855]).

TYPE MATERIAL. — **Malaysia** • Pulo Pinang; s.d.; *Didrichsen* 25; Lectotype designated by Gurgel *et al.* (2023): UPS-F-175963.

SPECIMENS EXAMINED. — **Brazil** • Amazonas, São Gabriel da Cachoeira, Comunidade de Itacoatiara-Mirim; 07.V.2019; T.S. Cabral, E.S. Andriolli, N.K. Ishikawa leg.; T.S. Cabral *et al.* 72; INPA-Fungos 297904.

SUBSTRATE. — On a fallen trunk of a deciduous tree.

DESCRIPTION

Basidiome perennial, gregarious to cespitose, ranging from dimidiate to imbricate, with its attack on the substrate widely adhered to semistipitate, 32–45 mm diameter × 21–39 mm width × 4–9 mm thickness, coriaceous and rigid. Pileus surface smooth, wrinkled, bluish, slightly shiny becoming dull with age, cinnabar red ($Y_{90}M_{90}C_{30}$) with grayish black spots ($N_{99}C_{99}Y_{00}$). Margin thick, obtuse, continuous and concolor with the pileus surface. Context and pileus surface continuous in cross-section, compact, 2–6 mm thick, cinnabar ($Y_{90}M_{80}C_{10}$) to red cinnabar ($Y_{90}M_{90}C_{30}$) and with homogeneous zones dark cinnabar ($Y_{90}M_{90}C_{10}$) and light cinnabar ($Y_{90}M_{70}C_{10}$), reflecting developmental stages. Line between context and hymenophore absent. Surface of the pores of the hymenophore

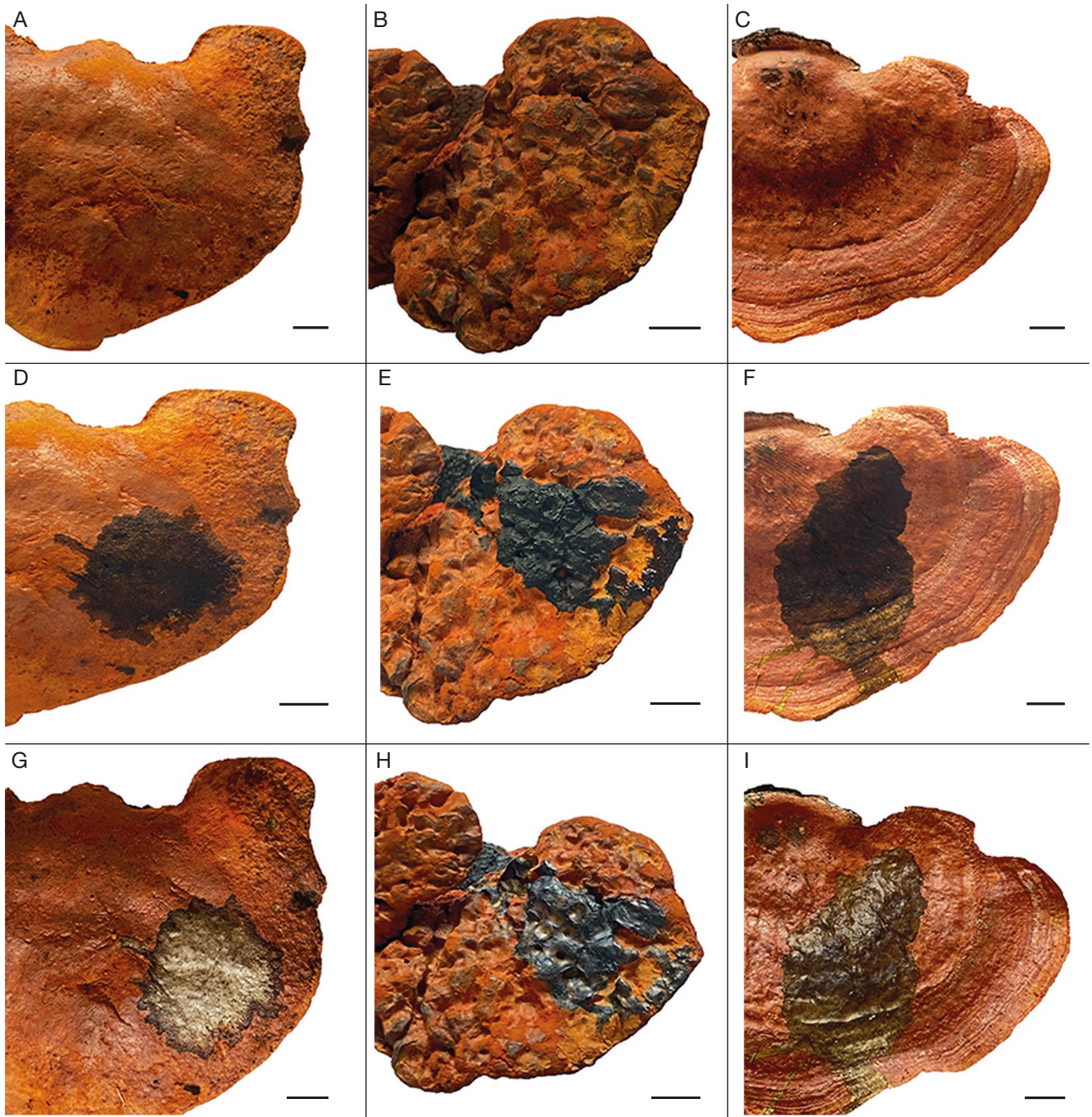


FIG. 9. — Reaction to KOH 5% in *Pycnoporus* P.Karst. specimens: **A–C**, basidiomes without reagent; **D–F**, immediately after application; **G–I**, after 24 hours, dried basidiomes. **A, D, G**, *Pycnoporus amazonicus* Gurgel & T.S.Cabral, sp. nov.; **B, E, H**, *Pycnoporus puniceus* (Fr.) Ryvarden; **C, F, I**, *Pycnoporus sanguineus* (L.: Fr.) Murrill. Scale bars: 1 cm.

dark orange red ($Y_{90}M_{80}C_{10}$); pores irregular to angular, 1–3 pores per mm, 0.3×0.7 mm diameter; dissepiment thick, entire and concolor to the pore surface; tube thick, entire and concolor to the pore surface. Macrochemical reaction occurs when adding 5% KOH, resulting in a color change to black permanently in basidiome. Hyphal system trimitic. Pileus surface composed of hyphae similar to the context. Context composed of generative hyphae thin-walled, with frequent clamps, rarely branched, 3–5 μ m diameter, hyaline to yellowish

in 5% KOH, CB-; IKI-; skeletal hyphae dominating, thick-walled, non-septate, unbranched, straight or slightly tortuous, 3–7 μ m diameter, hyaline to yellowish in 5% KOH, CB-; IKI-; binding hyphae thick-walled, non-septate, branched with short branches, 3–5 μ m diameter, hyaline to yellowish in 5% KOH and CB-; IKI-. Trama of the tubes composed of hyphae similar to the context; skeletal hyphae, 3–5 μ m diameter; binding hyphae more conspicuous than context, 1–4 μ m diameter. Hyphae with orange crystals predominate

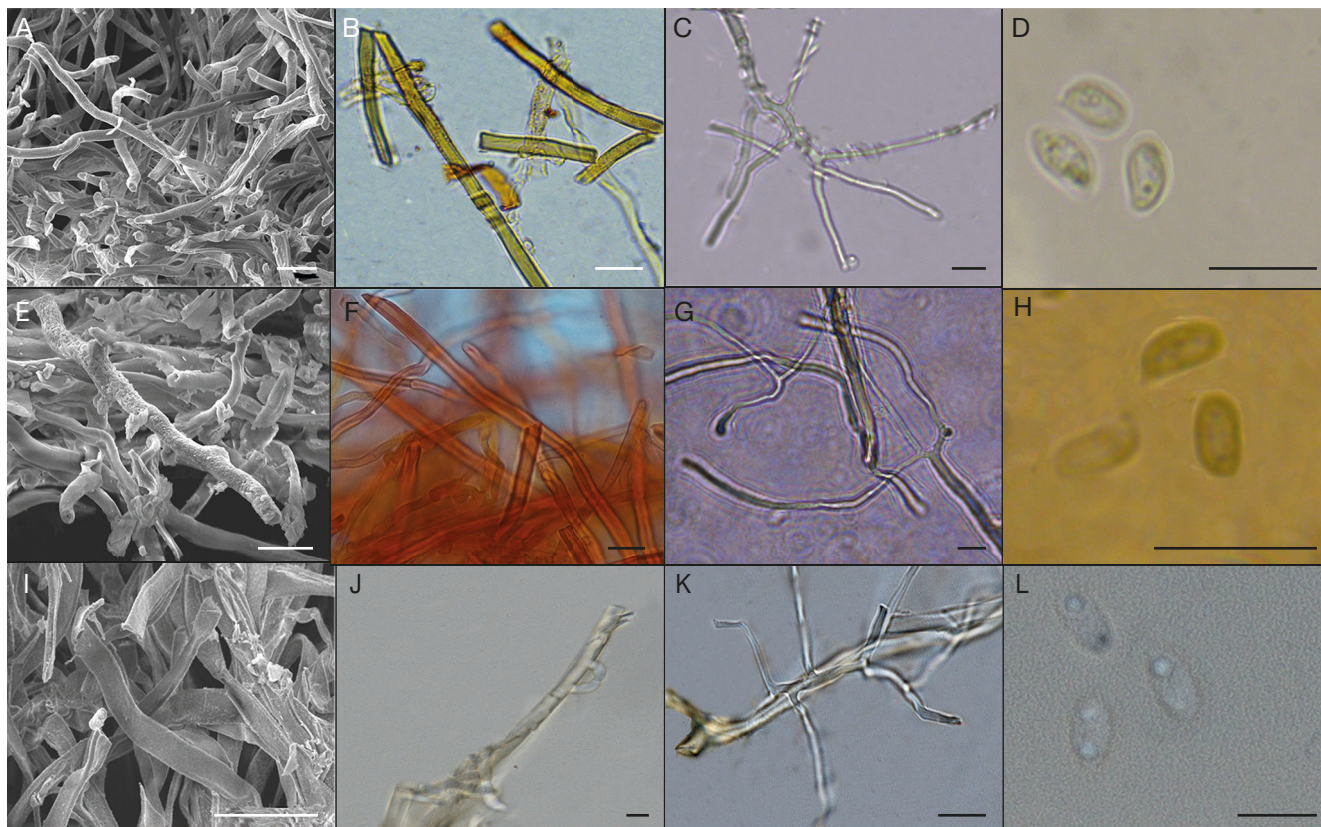


FIG. 10. — Microscopic view of hyphae and basidiospores in *Pycnoporus* P.Karst. **A-D**, *Pycnoporus amazonicus* sp. nov.: **A**, generative hyphae in SEM (arrows) (Holotype, INPA-Fungi 295581); **B**, skeletal hyphae in 5% KOH (Holotype, INPA-Fungi 295581); **C**, binding hyphae in 5% KOH (Holotype, INPA-Fungi 295581); **D**, basidiospores in 5% KOH (Paratype, INPA-Fungi 295551). **E-H**, *Pycnoporus puniceus* (Fr.) Ryvarden (INPA-Fungi 297904): **E**, generative hyphae, with details of the pigments (arrow) (SEM); **F**, skeletal hyphae in Congo Red; **G**, binding hyphae in 5% KOH; **H**, basidiospores in 5% KOH. **I-L**, *Pycnoporus sanguineus* (L.: Fr.) Murrill. **I**, skeletal hyphae in SEM (arrow) (UFRN-Fungos 175); **J**, generative hyphae with connecting clamps (arrow), in 5% KOH (URM 48716); **K**, binding hyphae in 5% KOH (UFRN-Fungos 48716); **L**, basidiospores in 5% KOH (URM 93314). Scale bars: A-D, F-H, J, K, 10 μ m; E, L, 5 μ m; I, 20 μ m. SEM photos provided by: CMABio-Centro Multiusuário para Análise de Fenômenos Biomédicos da UEA.

in all parts of the basidiomata, 2-3 μ m diameter, hyaline in 5% KOH, CB-; IKI-. Basidium clavate, 10-13 $\times$ 5-6 μ m, with basal clamp, four sterigmata, hyaline in 5% KOH, CB-; IKI-. Basidiospores 4.97-7.07 $\times$ 2.46-4.78 μ m ($x = 6.0 \pm 0.6 \times 3.5 \pm 0.6$; $Q_m = 1.7$), elongated, smooth, slightly curved, hyaline in 5% KOH, CB-; IKI-.

NOTES

Pycnoporus puniceus is a rare species with a known distribution in Africa, India, Malaysia, and New Caledonia (Lesage-Meessen *et al.* 2011). This study expanded its distribution to Brazil. This species appears as a strongly supported clade (PP = 1) (Fig. 4) in our phylogenetic analysis, and its cinnabar red coloration and irregular pores (1-3 per mm) stand out compared to other species in the genus.

Pycnoporus sanguineus (L.) Murrill (Figs 8; 9C, F, I; 10I-L).

Bulletin of the Torrey Botanical Club 31 (8): 421 (Murrill 1904). — *Boletus sanguineus* L., *Species Plantarum: exhibentes plantas rite cognitae*,

ad genera relatas, cum differentiis specificis, nominibus trivialibus, synonymis selectis, locis natalibus, secundum systema sexuale digestas: 1646 (Linnaeus 1763). — *Polyporus sanguineus* (L.) Fries, *Systema mycologicum*: 321 (Fries 1821). — *Microsporium sanguineus* (L.) Kuntze, *Revisio Generum Plantarum*: 497 (Kuntze 1898). — *Trametes sanguinea* (L.) Lloyd, *Index of the Mycological notes*: 1291 (Lloyd 1924). — *Trametes cinnabarina* var. *sanguinea* (L.) Kavina & Pilát, *Atlas des champignons de l'Europe*: 319 (Kavina & Pilát 1936). — *Coriolus sanguineus* (L.) Cunningham, *Plant Diseases Division Bulletin* 81: 17 (Cunningham 1949). — *Fabiosporus sanguineus* (L.) Zmitrovich, *Mycena* 1 (1): 93 (Zmitrovich 2001).

TYPE MATERIAL. — Suriname • around Capoerica; 3.IX.1755; *D. Rolander s.n.*; Lectotype designated by Moraes *et al.* (2014): LINN no. 1280.2.

SPECIMENS EXAMINED. — Brazil • Acre, Cruzeiro do Sul, Serra da Moa; 24.VI.1971; G.T. Prance, P.J.M. Mass, K. Kubitzki, W.C. Steward, J.F. Ramos, W.S. Pinheiro leg.; *J.F. Lima 12412*; INPA-Fungos 30735 • Rio Branco, km 7 SE of Rio Branco on road to Porto Velho; 30.IX.1980; B. Lowy, S.R. Lowrie leg.; *V.M. de Souza 369BR*; INPA-Fungos 100222 • Amapá, Mazagão, Estação Experimental de Mazagão; 01.VI.1961; *P. Ledoux s/n*; URM 48716 • Amazonas, Barcelos; 25.I.2015; D.L. Komura, J.J.S. Oliveira, J.R. Barbosa leg.; *DLK15003*; INPA-Fungos 265422 • Rio Aracá; 27.I.2015; D.L. Komura, J.J.S. Oliveira, J.R. Barbosa leg.; *DLK15012*; INPA-Fungos 265147 • Borba, Comunidade Caiçara; 10.VI.2021;

D.L. Komura leg.; *DLK3230*; INPA-Fungos 288922 • Iranduba, Sítio Hatahara; 23.II.2020; *C.C.S. de Souza 62*; INPA-Fungos 295587 • Itacoatiara, Fazenda Aruanã, Km 215 Rodovia Torquato Tapajós-Itacoatiara; 25.X.2021; R.A.F. Gurgel leg.; *RAFG87*; INPA-Fungos 295565 • same data; R.A.F. Gurgel leg.; *RAFG112*; INPA-Fungos 295566 • same data; R.A.F. Gurgel leg.; *RAFG113*; INPA-Fungos 295567 • same data; R.A.F. Gurgel leg.; *RAFG114*; INPA-Fungos 295568 • Manaus, Balneário Paraíso Nova Vida, Ramal do Pau Rosa Km 8, Km 21; 26.III.2022; R.A.F. Gurgel leg.; *RAFG121*; INPA-Fungos 295572 • same data; R.A.F. Gurgel leg.; *RAFG122*; INPA-Fungos 295573 • Estação Experimental de Manejo Florestal ZF-2, Bionte, BL2; 28.VI.2012; D.L. Komura leg.; *DLK848*; INPA-Fungos 288929 • Estrada do brasileiro, Sítio UDV; 24.II.2020; *C.C.S. de Souza 76*; INPA-Fungos 295594 • same data; *C.C.S. de Souza 84*; INPA-Fungos 295598 • Instituto Nacional de Pesquisas da Amazônia Sede; 24.VI.2021; D.L. Komura leg.; *DLK3126*; INPA-Fungos 288925 • Reserva Biológica Cuieiras, Estação Científica; R.A.F. Gurgel leg.; *RAFG79*; INPA-Fungos 295561 • same data; R.A.F. Gurgel leg.; *RAFG82*; INPA-Fungos 295562 • same data; R.A.F. Gurgel leg.; *RAFG116*; INPA-Fungos X295569 • same data; R.A.F. Gurgel leg.; *RAFG117*; INPA-Fungos 295570 • Reserva do Cuieiras; 03.VI.2019; D.L. Komura leg.; *T.G. Morbach DLK2665*; INPA-Fungos 288927 • Reserva Biológica do Cuieiras, Base Alto Cuieiras; 22.VI.2019; *N.K. Ishikawa 67*; INPA-Fungos 295574 • same data; *N.K. Ishikawa 68*; INPA-Fungos 295575 • same data; 22.VI.2019; *N.K. Ishikawa 80*; INPA-Fungos 295576 • same data; R.A.F. Gurgel leg.; *RAFG69*; INPA-Fungos 295560 • Tarumã Açú, próximo ao posto Vivenda Verde; 25.IV.2021; *C.C.S. de Souza 60*; INPA-Fungos 295585 • Universidade Federal do Amazonas, in front of FVA; 10.X.2021; R.A.F. Gurgel leg.; *RAFG86*; INPA-Fungos 295564 • Manicoré, Campinarana do Barro Alto; 12.XI.2019; D.L. Komura, M.R. Pereira, J.R. Costa-JR., D. Cerqueira leg.; *DLK2869*; INPA-Fungos 288923 • same data; Bairro Santo Expedito; 29.IV.2021; *C.A. Coelho 638*; INPA-Fungos 288920 • same data; Ramal Brasil, Sítio do Ranolfo; 29.IV.2021; *C.A. Coelho 639*; INPA-Fungos 288921 • Novo Airão, Parque Nacional do Jaú, parcela 3 incendiada; 23.IX.2017; J.J.S. de Oliveira, M.M.S. Pombo C.E. Zartman leg.; *JO835129*; INPA-Fungos 295582 • Anavilhanas Jungle Lodge; 15.IX.2021; J.J.S. de Oliveira e R.H. Nascimento leg.; *JO161989*; INPA-Fungos 295583; 16.II.2022; *J.J.S. de Oliveira, N.K. Ishikawa e R.E. Freitas* leg.; *JO1725123*; INPA-Fungos 295584 • Presidente Figueiredo, Ramal da Boa Esperança, Sítio do Sr. Braga e Joana; 09.III.2020; D.L. Komura; F.M. Costa, A. Tavares leg.; *DLK3026*; INPA-Fungos 288924 • RDS do Uatumã; 23.X.2020; D.L. Komura leg.; *DLK3087*; INPA-Fungos 288926 • Cachoeira da Asrama; 25.VIII.2021; R.A.F. Gurgel leg.; *RAFG65*; INPA-Fungos 295559 • Santo Antônio do Iça; 23.VII.2020; *C.C.S. de Souza 85*; INPA-Fungos 295599 • same data; *C.C.S. de Souza 75*; INPA-Fungos 295593 • same data; *C.C.S. de Souza 78*; INPA-Fungos 295596 • same data; *C.C.S. de Souza 61*; INPA-Fungos 295586 • same data; *C.C.S. de Souza 70*; INPA-Fungos 295590 • *ibidem*; 23.VII.2020; *C.C.S. de Souza 81*; INPA-Fungos 295597 • São Gabriel da Cachoeira, Comunidade Itacoatiara Mirim; 05.IV.2013; D.L. Komura, D.B.O. Cardoso, J.A. Correia da Silva leg.; *DLK1141*; INPA-Fungos 288928 • São Sebastião do Uatumã, RDS Uatumã, next to Torre ATTO; 20.III.2022; R.A.F. Gurgel leg.; *RAFG120*; INPA-Fungos 295571 • Tefé, Instituto Federal do Amazonas; 27.I.2021; *E.D. Koch 66*; INPA-Fungos 295579 • Bahia, Santa Teresinha, Serra da Jibóia; 23.IX.2010; *T.B. Gilbertoni TGB34*; URM 83471 • Ceará, Crato, Flona Nacional do Araripe, Brejo de Altitude; 15.V.2012; C.R.S. Lira leg.; *CL825*; URM 83799 • Fortaleza, Parque Estadual do Cocó; 23.VII.2019; *C.C.S. de Souza 64*; INPA-Fungos 295589 • same data; 23.VII.2019; *C.C.S. de Souza 77*; INPA-Fungos 295595 • Fortaleza, Universidade Federal do Ceará, Museu Casa do José de Alencar; 05.VII.2020; *C.C.S. de Souza 73*; INPA-Fungos 295592 • Maranhão, Cidelândia, Povoado do Ciriaco, Reserva Extrativista do Ciriaco; 30.VII.2013; L.S. Araujo-Neta, R.S. Nogueira leg.; *26AN-MA*; URM 85566 • Mato Grosso, Aripuanã, Estrada para

Mineração São Francisco, km 41; 19.IV.1985; *K.F. Rodrigues 208*; INPA-Fungos 128951 • Minas Gerais, Ituiutaba, Parque Municipal do Goiabal; 27.IV.2016; N.C. Carvalho, L.M. Rocha leg.; *NCC4*; URM 93314 • Santana do Riacho, Serra do Cipó, Trilha dos Escravos; 25.XII.2019; *C.C.S. de Souza 71*; INPA-Fungos 295591 • Cachoeira Grande; 26.XII.2019; *C.C.S. de Souza 63*; INPA-Fungos 295588 • Pará, Oriximiná, Floresta Nacional de Saracá-Taquera; 25.I.2022; *D.M. Couceiro 124*; INPA-Fungos 295546 • Medicilândia, 85 Norte; 26.VI.2022; R.J.S. Dalman leg.; *RJS223126*; INPA-Fungos 295549 • Paraíba, Santa Teresinha, Fazenda Tamanduá; 23.III.2008; *E.P. Fazolino s/n*; UFRN-Fungos 489 • Paraná, Mauá da Serra, Sítio Komura; 15.I.2021; D.L. Komura leg.; *DLK3272*; INPA-Fungos 296004 • Tamarana, Fazenda Pinheiros, no estacionamento da cachoeira; 18.IX.2021; N.K. Ishikawa leg.; *N.K. Ishikawa 111*; INPA-Fungos 295578 • same data; *N.K. Ishikawa 88*; INPA-Fungos 295577 • Pernambuco, Buíque, Parque Nacional Vale do Catimbau, 16.IV.2009; *J.J.S. Oliveira s/n*; UFRN-Fungos 1039 • Piauí, Caracol, Serra das Confusões; 15.III.2012; C.R.S. Lira leg.; *CL595*; URM 83640 • Rio Grande do Norte, Natal, Parque Estadual Dunas de Natal; 10.IX.2005; I.G. Baseia leg.; *P.P.T. Lacerda s/n*; UFRN-Fungos 1743 • same data; 13.VI.2006; B.D.B. Silva, A.G. Leite, I.G. Baseia leg.; *s/n*; UFRN-Fungos 250 • same data; 12.VII.2008; *E.P. Fazolino s/n*; UFRN-Fungos 756 • same data; 28.X.2010; M. Capelari leg.; *I.G. Baseia s/n*; UFRN-Fungos 33 • same data; 28.X.2010; *M. Capelari leg.*; *I.G. Baseia s/n*; UFRN-Fungos 175 • Universidade Federal do Rio Grande do Norte, next to Centro de Biotecnologias; 6.II.2021; R.A.F. Gurgel leg.; *RAFG58*; INPA-Fungos 295557 • same data; R.A.F. Gurgel leg.; *RAFG59*; INPA-Fungos 295558 • Estuário do Rio Potengi; 12.IX.2005; M.M.B. Barbosa leg.; *J.J.S. Oliveira s/n*; UFRN-Fungos 604 • Parnamirim, Mata do Jiqui; 16.VI.2006; *P.P.T. Lacerda s/n*; UFRN-Fungos 252 • same data; 04.VII.2008; E.P. Fazolino; M.A. Silveira leg.; *M.P.G. Pinheiro s/n*; UFRN-Fungos 753 • Pium, Vale Encantado; 07.VII.2021; R.A.F. Gurgel leg.; *RAFG83*; INPA-Fungos 295563 • Serrinha, Fazenda Guagirú; 18.IV.2010; *T.F.R. Pessoa s/n*; UFRN-Fungos 1662 • Rondônia, Coacal, próximo as Fazendas; 03.XI.2021; *C.C.S. de Souza 115*; INPA-Fungos 295600 • Roraima, Vicinity of Auaris; 23.VII.1974; G.T. Prance, O. Fidalgo, B.W. Nelson leg.; *J.F. Ramos 21320*; INPA-Fungos 45299; Estrada Manaus-Caracará, km 328; 16.XI.1977; I. de J. Araújo, M.A. Sousa, J. Bernardi, K.P. Dumont, D. Hosford, G. Samuels leg.; *I. de J. Araújo et al. 403*; INPA-Fungos 76930 • same data; 16.XI.1977; I. de J. Araújo, M.A. Sousa, J. Bernardi, K.P. Dumont, D. Hosford, G. Samuels leg.; *I. de J. Araújo 413*; INPA-Fungos 76940 • Santa Catarina Penha; 29.XII.2020; *E.D. Koch 74*; INPA-Fungos 295580 • São Paulo, Buri, Instituto Brasileiro do Meio Ambiente e dos Recursos Naturais Renováveis (IBAMA); 13.VII.1987; M.A. de Jesus leg.; *M.A. de Jesus 1120*; INPA-Fungos 186295.

SUBSTRATE. — Grows on various types of deadwood, mainly in open sunny places.

DESCRIPTION

Basidiome annual to perennial, solitary, gregarious to cespitose; ranging from dimidiate, flabelliform, spatulate, semicircular, infundibuliform, with attack on the substrate ranging from strongly adhered, semistipitate to stipitate, 70–124 mm diameter × 47–85 mm width × 2–4.5 mm thick, coriaceous. Stipe 6–19 mm width × 2–4 mm thick, solid, concolor to pileous. Pileus surface coriaceous when damp, becoming stiff when dry, velvety and glossy when young, glabrous and striated with age, reddish orange ($N_{00}Y_{99}M_{90}$) to vivid orange ($N_{00}Y_{90}M_{70}$), with alternating zones of yellowish white ($N_{00}Y_{20}M_{00}$) to orange ($N_{00}Y_{90}M_{60}$), becoming yellowish white ($N_{00}Y_{20}M_{00}$) over the entire surface at high temperatures and when old. Margin thin, acute, entire to irregular, sometimes tomentose,

yellowish orange (N₀₀Y₉₉M₅₀) to whitish yellow (N₀₀Y₂₀M₀₀). Context and surface of the pileus continuous in cross section, floccose to fibrous, shiny, 1.4–3 mm thick, pale yellow (N₀₀Y₃₀M₀₀) and light orange (N₀₀Y₈₀M₄₀) zones, radially separating, reflecting the stages of development. Line between the context and the hymenophore sometimes present, pale yellow (N₀₀Y₃₀M₀₀). Surface of the pores of the hymenophore intense reddish orange (N₀₀Y₉₉M₉₀) to moderate reddish orange (N₀₀Y₉₀M₈₀); pores circular to angular, tomentose and serrated walls, 5–8 pores per mm, 0.1 × 0.3 mm diameter; dissepiment thick when young, becoming thinner with age, concolor to the pore surface; tube circular, 1–2 layers 1–1.5 mm deep × 0.3 mm wide, light orange (N₀₀Y₈₀M₀₀) and whitish yellow (N₀₀Y₂₀M₀₀). Macrochemical reaction occurs when adding 5% KOH, resulting in rapid color change from black to greenish brown in part of the basidiome. Hyphal system trimitic. Pileus surface similar to the context. Context composed of generative hyphae thin-walled, with frequent clamps, rarely branched, 1–4 µm diameter, hyaline to yellowish in 5% KOH, CB–; IKI–; skeletal hyphae dominate, straight or slightly tortuous, thick-walled, unbranched, 2–6 µm diameter, hyaline to yellowish in 5% KOH, non-cyanophilous and non-amyloid; binding hyphae thick-walled, non-septate, branched with short branches, 2–3 µm diameter, yellowish in 5% KOH, CB–; IKI–. Trama of the tubes composed of hyphae similar to the context. Hyphae with orange crystals predominate in all parts of the basidiome, 2–4 µm diameter, hyaline in 5% KOH, CB–; IKI–. Basidium clavate, 11–15 × 5–6 µm, with basal clamp, four sterigmata, hyaline in 5% KOH, CB–; IKI–. Basidiospores 4.02–5.96 × 1.58–3.62 µm ($x = 4.79 \pm 0.5 \times 2.5 \pm 0.4$; Qm = 1.9), elongated, smooth, slightly curved, hyaline in 5% KOH, CB–; IKI–.

REMARKS

This species presents basidiomata whose characters, such as pileus colours, texture and zoning, change depending on environmental conditions. These changes can lead to misidentifications, especially with morphologically similar species, such as *P. coccineus*, which has an orange to reddish-orange basidiome and areas with colors similar to the pileus. *Pycnoporus coccineus* differs from *P. sanguineus* by having a basidiome with a soft aspect and 3–5 pores per mm with thick walls. *Pycnoporus sanguineus* has an ample worldwide distribution, as can be observed by the distribution of its sequences in the phylogenies of ITS (Fig. 4) and, for Brazil, it can be found in almost all states, of which here we report a new record for the state of Roraima.

DISCUSSION

Our analyses extend the sample coverage for phylogeny in terms of number of specimens, species and geographical distribution for *Pycnoporus* and allocate the specimens into a monophyletic clade, with *Trametes versicolor* as the basal group (dataset A, Fig. 2), following what was observed in Lesage-Meessen *et al.* (2011) and Welti *et al.* 2012.

Although with similar morphological concepts, *Pycnoporus* and *Trametes* can be differentiated by the reddish-orange hue of the basidiomata, hyphae with orange granules and the presence of a pseudostipe or stipe in *Pycnoporus*; whereas in *Trametes*, the basidiomes have brown tones, a white to cream and sometimes brown context, no hyphae with orange granules and no pseudostipe or stipe (Ryvarden 1991; Ryvarden & Gilbertson 1994; Welti *et al.* 2012). These colorations in *Pycnoporus* are the result of the synthesis of various pigments, such as cinnabarin, cinnabarinic acid and tramesanguin and pycnoporin (Téllez-Téllez *et al.* 2016), which are synapomorphies of the group and can be used to delimit the genus.

Justo & Hibbett (2011) used a dataset of five molecular markers and placed the species of *Pycnoporus* and other related genera in the trametoid clade, classifying them under a single generic name, *Trametes* sensu stricto, reviving nomenclature combinations such as *Trametes cinnabarina*, *Trametes sanguinea* (L.: Fr) and *Trametes punicea* Fr. The decision to accept *Pycnoporus* sensu lato vs *Trametes* s. lat. would also have been possible provided that *Cubamyces Murrill* (synonym of *T. cubensis* (Mont.) Sacc.) was accepted as a sister group of *Pycnoporus*. Recently, *Cubamyces* was recognized by Lücking *et al.* (2020) as a separate genus, grouping four species. Although *Pycnoporus* presents distinct morphological characteristics and is a monophyletic group, our results alone are not sufficient to make the decision as to whether or not to segregate the genus *Trametes*. We believe that other studies need to be carried out that focus on other supposed genera, such as Lücking *et al.* (2020) with *Cubamyces*, involving different data sources in addition to DNA and morphology, for a better understanding of the circumscription of the taxa.

With the phylogenetic analyses, it was possible to recover the clades corresponding to the known species of the genus and putative species not yet known, with clades similar to those found in Lesage-Meessen *et al.* (2011). In both, ITS and concatenate analyses, *P. puniceus* and *P. cinnabarinus* appear to have the same phylogenetic position; however, there is uncertainty about the relationships between the other species and clades. *Pycnoporus puniceus* presents the most divergent sequences within the group, and encompasses Tropical specimens from Central Africa and Australia, although it was initially described for the paleotropical region (Malaysia) (Gurgel *et al.* 2023). In the topology of ITS (Fig. 4), it is possible to observe the formation of clades in *P. puniceus* from different locations, as one from Thailand (PP = 0.94) and another from Gabon, Cuba, Brazil and Australia (PP = 1); however, we cannot infer whether all refer to *P. puniceus* or a new species, due to the lack of additional data, even with the presence of the reference sequence of the species. This situation is repeated in other clades, which may indicate a possible wide geographical distribution for the species, except for *P. coccineus*, which seems to be restricted to the region of Australasia, Polynesia (type locality) and Austria. However, these clades deserve attention in future work since they may also represent different species.

TABLE 3. — Comparison of morphological characters between *Pycnoporus* P.Karst. species.

Characteristics	<i>P. amazonicus</i> Gurgel & T.S.Cabral, sp. nov.	<i>P. cinnabarinus</i> (Jacq.) P.Karst.	<i>P. coccineus</i> (Fr.) Bondartsev & Singer	<i>P. puniceus</i> (Fr.) Ryvarden	<i>P. sanguineus</i> (L.) Murrill
Basidiomata	Dimidiate to semicircular, broadly attached to applanate, soft and corky to coriaceous, semistipitate	Dimidiate to sessile and sometimes with umbo, laterally extended, large and bulky	Dimidiate to sessile, broadly attached, corky to coriaceous	Dimidiate to imbricate, broadly attached, corky and rigid, semistipitate	Varied shapes, corky to coriaceous, broadly attached, stipitate, semistipitate
Size (mm) diam. × width × thick	115 × 66 × 5	60 × 100 × 170	50 × 150 × 10	45 × 39 × 9	124 × 85 × 4.5
Pileus surface	Azonate, crusty to glabrous, velvety to tomentose, and shining when young	Azonate, tomentose to glabrous, velvety in young	Azonate, velvety	Azonate, wrinkled to glabrous, slightly shining to dull	Zonate, glabrous and shining, velvety when young, striated and hard with age
Color pileus	Orange to matte orange, becoming yellowish white in older	Moderate orange becoming brownish orange	Moderate orange becoming moderate reddish orange	Cinnabar red with gray black	Reddish orange to strong orange, zones yellowish white and orange
Margin	Acute to obtuse, thick, concolor to pileus	Obtuse to acute, thick, brownish orange	Obtuse, concolor with pileus to deep orange yellow	Obtuse, thick, continuous and concolor with pileus	Acute, thin, yellowish orange to white
Context	Fibrous and soft-compactus, distinct surface and context, brownish with band orange and cream, 3 mm thick	Floccose to fibrous and corky, continuous surface and context, with zones lighter and darker, 166 mm thick	Floccose to fibrous and soft, with zones orange pale, with white and moderate orange yellow, 7.5 mm thick	Fibrous and compactus, continuous surface and context, cinnabar to red cinnabar, with zones darker and lighter, 6 mm thick.	Floccose to fibrous, continuous surface and context, shining, pale yellow and light orange, separating in zones, 3 mm thick
Line under context	Grayish brown line between context and hymenophore	Not related	Not related	Without line	Sometimes a white line between context and hymenophore
Hymenophore	Surface bright orange to moderate reddish orange; tubes about 2.5 mm, pale orange	Vivid reddish orange to strong orange; tubes about 4 mm thick	Concolor to pileus, but in parts moderate reddish orange turning moderate orange; tubes about 2.5 mm thick	Surface orange red; tubes about 2.5 mm thick, concolor to pore surface	Surface reddish orange to moderate reddish orange; tubes about 1.5 mm thick, pale orange with whitish yellow
Pores	3-4 (-5) per mm, thin walls, angular to irregular	1-3 (-4) per mm, very thick walls leaving the pores smaller in diameters, angular to circular	3-4 (-5) per mm, thick walls turning thinner with age, circular	1-3 per mm, thick walls, irregular to angular	(-5) 6-8 per mm, thin to thick wall, circular to angular, tomentose and serrated walls
5% KOH	Quick color change black to greenish brown	Not related	Not related	Changing to black	Quick color change black to greenish brown
Hyphal system	Generative hyphae up to 2-4 µm diam.; Skeletal hyphae up to 3-7 µm diam.; Biding hyphae more abundant in trama and in transition between context and tubes, 2-4 µm ; and hyphae with orange granules	Generative hyphae up to 1-3 µm diam.; Skeletal hyphae up to 4-7 µm diam.; Biding hyphae more abundant in trama and in transition between context and tubes, 2-4 µm; and hyphae with orange granules	Generative hyphae up to 2-3 µm diam.; Skeletal hyphae up to 3-5 µm diam.; Binding hyphae up to 3-4 µm, branches 1-2 µm ;and hyphae with orange granules	Generative hyphae 3-5 µm diam.; Skeletal hyphae up to 3-7 µm diam.; Binding hyphae more abundant in trama, up to 4 µm; and hyphae with orange granules	Generative hyphae up to 1-4 µm diam.; Skeletal hyphae 2-6µm; Binding hyphae up to 1-3µm; and hyphae with orange granules
Basidiospores	Elongated, flattened on one side, slightly curved, smooth 5.7-7.9 × 3.0-4.8 µm;	Short cylindric to cylindric, flattened on one side, slightly curved, smooth 4.6-5.9 × 2.0-2.6 µm;	Short cylindric, slightly flattened on one side or slightly curved, 4.0-5.2 × 2.0-2.3	Elongate, flattened on one side, slightly curved, smooth walls, 4.9-7.0 × 2.4-4.7 µm	Elongate, flattened on one side, slightly curved, 4.0-5.9 × 1.5-3.6 µm
Reference	Present study	Jacquin 1776; Fries 1821; Nobles & Frew 1962; Lectotype analysis	Fries 1851; Bondartsev & Singer 1941; Nobles & Frew 1962; Lectotype analysis	Present study	Present study

The sequences of the specimens belonging to *Pycnoporus* sp. were grouped into a well-supported and distinct clade in all the phylogenetic trees. The phylogenetic position of *Pycnoporus* sp. seemed uncertain in the topology of the ITS tree (Fig. 4), where there is no resolution of this relationship. However, in the concatenated tree (Fig. 3), it is a sister to the clades with *Pycnoporus sanguineus*, *Pycnoporus* sp. and *Pycnoporus coccineus*. Moreover, in the Polyporales tree (Fig. 2), *P. amazonicus* Gurgel & T.S.Cabral, sp. nov. appears as a sister group to *P. puniceus*, although it also does not show resolution regarding the relationships of the other species. *Pycnoporus amazonicus* Gurgel & T.S.Cabral, sp. nov. is morphologically distinguishable from the other species (see details in taxonomy and Table 3) and is so far composed by Brazilian specimens.

Other clades were formed, which due to the absence of additional data for a decision at the species level, mainly the morphological data, we prefer to treat this clade as *Pycnoporus* sp. until sufficient data are obtained for its definition. Regarding these clades, by concatenating the data (dataset B, Fig. 3), *Pycnoporus* sp. 1 has no support value, while *Pycnoporus* sp. 2 and *Pycnoporus* sp. 3, were recovered by analyzing dataset B and C (as *Pycnoporus* sp. 1 and *Pycnoporus* sp. 2 in the ITS dataset, respectively) with highly supported in both analyses (Figs 3; 4). These specimens lack morphological data, and for a more accurate delimitation, it is necessary that the specimens in this clade must undergo integrative taxonomy, which may result in the delimitation of new species for Asia and Oceania (Paleotropics).

Our divergence time results for Polyporaceae are in agreement with those of Song & Cui (2017), who concluded that the diversification of *Laetiporus* Murrill (Polyporales) occurred during the early Miocene (20.17 ± 0.12 Mya), and here we find, on average, 18.44 Mya for this process (Fig. 5). Similarly, the maximum crown age (14.35 Mya) for *Pycnoporus* is also around Miocene, but the stem age indicates a time span of 25 Myr since the arising of the genus and its diversification. This period was characterized by rapid global cooling during the Eocene-Oligocene transition, with major extinctions and species turnover in plants and animals (Coxall & Pearson 2007; Fattorini 2021). On the other hand, the diversification of *Pycnoporus* coincides with the Middle Miocene Thermal Maximum (16–14 Mya), where the global temperatures were warmer and Earth was highly forested, and conditions favored fauna and flora species arising (Scotese *et al.* 2021; Steinthorsdottir *et al.* 2021). Similar patterns were regionally found for fungi (Romero *et al.* 2021), thus the Miocene paleoclimate may also have influenced species emergences in *Pycnoporus*. However, more precise biogeographical inferences are only possible with additional data and analysis. At the species level, with the inclusion of other gene regions or genomic data in the analyses of phylogeny with divergence time, allied to the correct identification of the species, it will be possible to understand how some of the species in *Pycnoporus* are widely distributed geographically and which historical biogeographic events have influenced this current distribution. Interestingly, the specimens collected in Asia

appear in all clades delimited here at the species level, which suggests probable long-distance dispersal. Additionally, the influence of human activities can also be considered when studying the current pattern of geographical distribution, such as the introduction of exotic species and deforestation.

SPECIES DIVERSITY FOR *PYCNOPORUS* IN BRAZIL

In Brazil, specimens of *Pycnoporus* are widely reported in GBIF (2024) and *P. sanguineus* was, until the present study, the only species in the country registered for the genus (Flora do Brasil 2024).

Pycnoporus sanguineus has a wide geographical distribution, with records for Southwest Asia, Africa (Madagascar & Benin) and Central and South America, as observed by the specimens grouped in the phylogenetic analysis of the present study (Figs 3; 4). Among the descriptions reported for *P. sanguineus*, there are variations between some characters, such as the number of pores per mm and the shape and size of basidiospores. Nobles & Frew (1962) reported 4–6 pores per mm and basidiospores $4.5.2 \mu\text{m} \times 2.2.6 \mu\text{m}$ in specimens from Louisiana, India, Kenya, Tanganyika, Holland, New Guinea, Brazil and South Africa. For the Neotropics, Ryvarden (2016) reports the same number of pores, and slightly larger cylindrical basidiospores, $5.6 \mu\text{m} \times 2.2.5 \mu\text{m}$. For Brazilian specimens, our description is in accordance with Gugliotta & Bononi (1999) and Silva & Gibertoni (2006), who report specimens with angular pores of 5–7 per mm and cylindrical to ellipsoid basidiospores between $3.5.6 \mu\text{m} \times 2.3.5 \mu\text{m}$ for the Atlantic Forest. Also, Neves *et al.* (2013) report specimens with 4–6 pores per mm, with cylindrical basidiospores of $5.6 \mu\text{m} \times 2.2.5 \mu\text{m}$ for the Brazilian semiarid region. In contrast, Abrahão *et al.* (2009) described *P. sanguineus* for São Paulo (Atlantic Forest) and reported a greater variation of 2–8 pores per mm and cylindrical basidiospores of $3.5.6.2 \mu\text{m} \times 1.2.5 \mu\text{m}$. The disparity found in the morphological data demonstrates a wide phenotypic plasticity in the specimens of *P. sanguineus*, which may be related to the occupation by the species of different habitats under different edaphoclimatic conditions, and, therefore, to the adaptive ability.

Here, we reaffirm the presence of *P. sanguineus* for Brazil through morphological similarities with type material, analysis of the protologue of the basionym and the sanctioned drawing (Gurgel *et al.* 2023), in addition to the use of reference sequences according to the proximity to its type location (Suriname) (Murril 1907) and new sequences generated in this study. Nonetheless, *P. sanguineus* has already been reported for several Brazilian states (Flora do Brasil 2024), though we recorded this species for the first time for the state of Roraima.

Additionally, SpeciesLink (2024) records an exsiccate of *P. puniceus* for Brazil, which is reported in Soares (2017); however, no testimonial material was located according to the number and location reported. We analyzed a specimen whose sampling location was in São Gabriel da Cachoeira, Amazonas, Brazil, in which the morphological description,

pileus and context with cinnabar tones, 1-3 pores in the hymenophore, allied to our phylogenetic analysis, and identified it as *P. puniceus*. Thus, since the species was previously recorded for South America (French Guiana; GBIF 2024), we report it for the first time for Brazil.

The report of *P. amazonicus* Gurgel & T.S.Cabral, sp. nov., *P. puniceus*, and *P. sanguineus* is significant in terms of the genus's diversity in the country compared to the total diversity of the genus previously reported. However, more studies are still needed to document the genus's diversity in Brazil in areas where materials were not possible to obtain, such as the Pampa and Pantanal biomes.

CONCLUSION

The present study draws attention to a genus that have great biotechnological potential, *Pycnoporus*, but which are taxonomically underestimated and, although widely distributed, need conservation measures since they may reveal hidden diversity. Despite other authors opting for the synonymization with the genus *Trametes*, our study showed that there are morphological and phylogenetic evidence, as well as biochemical and nomenclatural characteristics that have been demonstrated in previous studies, that support *Pycnoporus* as a independent genus. Thus, it is advisable to perform an integrative taxonomic review of *Trametes* and synonymous genera to identify arguments that support the separation of the genera from *Trametes*, enabling the classification of the clade *Pycnoporus* and others. Finally, we want to point out that the inclusion of sequences of type specimens and other localities beyond the Neotropics, associated with other molecular markers, is necessary and can clarify the relationships of *Pycnoporus* species and, as demonstrated here, the proposition of scientific discoveries, new records and the biogeographical history of the genus.

Acknowledgements

The authors are grateful to all curators of the herbaria cited in this article (INPA-Fungos, URM, UFRN-Fungos) and to the additional collectors for the materials provided, especially Crisvaldo Cássio de Souza, Douglas Couceiro and Esteban Koch. We thank the Conselho Nacional de Desenvolvimento Científico e Tecnológico for providing a graduate fellowship, and for funding (PPBio 2023 (441288/2023-5) and PROTAX 2024 (445729/2024-4)). TSC is grateful to the Coordenação de Aperfeiçoamento de Pessoal de Nível Superior for providing a scholarship (CAPES 88882.317512/2019-01). CSC thank the post-doctoral research fellowship agreement CAPES/JBRJ, the agreement between CNPq and the Government of the State of Amazonas (Brasil) / Fundação de Amparo à Pesquisa do Estado do Amazonas (FAPEAM) (grant no. 01.02.016301.00757/2022-50) for providing the DCR fellowship, and Fundação Carlos Chagas Filho de Amparo à Pesquisa do Estado do Rio de Janeiro, programa "Pós-doutorado Nota 10-2024"

(FAPERJ, PDR-10-2024, grants no. E-26/200.379/2025 and E-26/200.380/2025). We are thankful to the Fundação de Amparo à Pesquisa do Estado do Amazonas (FAPEAM 01.02.016301.03240/2021-32) provided funding (process number 01.02.016301.03240/2021-32 of the edital no 007/2021-BIODIVERSA, process number 01.02.016301.03246/2021-00 of the edital no. 008/2021-PROSPAM, and PROSGRAD). This study was financed in part by the Coordenação de Aperfeiçoamento de Pessoal de Nível Superior-Brasil (CAPES)-Finance Code 001. The authors also thank the reviewers and the editor-in-chief for their valuable work.

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Submitted on 1 July 2024;
accepted on 8 November 2024;
published on 3 December 2025.

APPENDIX

APPENDIX 1. List of voucher materials and associated GenBank sequence.

Taxa	Voucher	Origin	nrITS	nrLSU	tef1a	rpb2
<i>Aurantiporus albidus</i>	CIEFAP-117	Argentina	KY948739	KY948848	–	–
<i>Bankera fuligineoalba</i>	REB-285	United States	JN135196	–	–	KF007978
<i>Bjerkandera adusta</i>	HHB-12826-Sp	United States	KP134983	KP135198	–	KP134913
<i>Byssomerulius corium</i>	FP-102382	United States	KP135007	KP135230	–	KP134921
<i>Candelabrochaete langloisii</i>	FP-110343-sp	United States	KY948793	KY948886	–	–
<i>Ceraceomyces americanus</i>	FP-102188	United States	KP135409	KP135277	–	KP134934
<i>Ceraceomyces serpens</i>	HHB-15692-Sp	United States	KP135031	KP135200	–	–
<i>Ceriporiopsis squamosus</i>	Cui 10595	China	KU189778	KU189809	KU189925	KU189988
<i>Ceriporiopsis carnegieae</i>	RLG-7277-T	United States	KY948792	KY948854	–	–
<i>Climacodon septentrionalis</i>	AFTOL-ID 767	–	AY854082	AY684165	AY885151	AY780941
<i>Cryptoporus volvatus</i>	DOM21791	–	–	AF393050	–	AY218479
<i>Daedalea africana</i>	O 15372	Kenya	KP171196	KP171216	KR610704	KR610795
<i>Daedaleopsis confragosa</i>	WD747	Japan	LC471201	–	–	AB368120
<i>Datronia mollis</i>	RLG6304	United States	JN165002	JN164791	JN164901	JN164872
<i>Datronia</i> sp.	Cui 10646	China	KC415186	KC415194	KX838429	KC415201
<i>Datronia</i> sp.	Dai11921	China	JX559272	JX559283	–	JX559320
<i>Dentocorticium portoricense</i>	He2161	United States	MF626356	MF626380	–	MF626397
<i>Dentocorticium sulphurellum</i>	T609	Canada	JN165015	JN164815	–	JN164875
<i>Earliella scabrosa</i>	PR1209	Puerto Rico	JN165009	JN164793	JN164894	JN164866
<i>Efibula americana</i>	FP-102165	United States	KP135016	KP135256	–	KP134916
<i>Epithele macarangae</i>	FP-150881	Belize	KY948713	KY948843	–	–
<i>Favolus acervatus</i>	Cui 11053	China	KU189774	KU189805	KU189920	KU189994
<i>Fomitella supina</i>	Miettinen 17695 (H)	United States	KY948711	KY948841	–	–
<i>Fomitopsis pinicola</i>	Cui 10312	China	KR605781	KR605720	KR610689	KR610780
<i>Fragifomes niveomarginatus</i>	Cui 10108	China	KR605778	KR605717	KR610684	KR610776
<i>Fragiliporia fragilis</i>	Dai 13080	China	KJ734260	KJ734264	KJ790245	KJ790248
<i>Funalia subgallica</i>	Dai6329	–	KC867386	KC867462	–	KX885086
<i>Ganoderma australe</i>	ZRL20151500	China	LT716076	KY418900	KY419088	–
<i>Grammothele aff. fuligo</i>	FP-150657	Belize	KY948716	KY948840	–	–
<i>Grammothelopsis subtropica</i>	Cui 9035 T	China	JQ845094	JQ845097	KF181124	–
<i>Grifola frondosa</i>	AFTOL-ID 701	–	AY854084	AY629318	AY885153	AY786057
<i>Haploporus odoratus</i>	Yuan 2365	China	KU941846	KU941870	KU941933	KU941916
<i>Hexagonia cucullata</i>	Dai 13894	China	KX880626	KX880664	KX880882	–
<i>Hexagonia tenuis</i>	Niemela-9032	Zambia	KY948842	KY948842	–	–
<i>Hirticrusta subradiata</i>	Cui 11035	China	KX900667	KX900717	KX900850	–
<i>Hydnophlebia chrysorhiza</i>	FD-282	United States	KP135338	KP135217	–	KP134897
<i>Hyphodermella rosae</i>	FP-150552	United States	KP134978	KP135223	–	KP134939
<i>Irpex lacteus</i>	DO_421/951208	Sweden	JX109852	JX109852	JX109911	JX109882
<i>Irpex rosettiformis</i>	Meijer3729	Brazil	JN649346	–	–	JX109875
<i>Ischnoderma resinatum</i>	FD-328	United States	KP135303	KP135225	–	KP134972
<i>Laetiporus sulphureus</i>	Dai 12154	Czech Republic	KF951295	KF951302	KR610752	KR610841
<i>Lenzitopsis</i> sp.	Yuan 2959 T	–	JN169799	JN169795	–	–
<i>Leptoporus mollis</i>	TJV-93-174-T	United States	KY948795	EU402510	–	–
<i>Lignosus hainanensis</i>	Dai 10670 T	China	NR154112	GU580886	–	–
<i>Lopharia cinerascens</i>	FP-105043sp	United States	JN165019	JN164813	JN164900	JN164874
<i>Megasporoporia bannaensis</i>	Dai 12306 T	China	JQ314362	JQ314379	KF494979	–
<i>Megasporoporiella lacerata</i>	Yuan 3880 T	–	JQ314377	JQ314395	KF286334	–
<i>Melanoderma microcarpum</i>	Cui 10970	China	KX900662	KX900712	KX900845	KX900813
<i>Meripilus giganteus</i>	FP-135344-Sp	–	KP135307	KP135228	–	KP134894
<i>Meruliopsis albostramineus</i>	HHB-10729	United States	KP135051	KP135229	–	KP134926
<i>Microporus xanthopus</i>	PEN79	–	–	AB368075	–	AB368133
<i>Neofavolus alveolaris</i>	Dai 11290	China	KU189768	KU189799	KU189913	KU189982
<i>Niveoporofores spraguei</i>	JV 0509/62	United States	KR605786	KR605725	KR610697	KR610788
<i>Perenniporia hainaniana</i>	Cui 6364	China	JQ861743	JQ861759	KF181138	–
<i>Perenniporiella chaqueniana</i>	MUCL 47647	Argentina	FJ411083	FJ393855	HM467609	–
<i>Phaeophlebiopsis caribbeana</i>	HHB-6990	United States	KP135415	KP135243	–	KP134931
<i>Phanerochaete chrysosporium</i>	FPL5175	–	AY854086	AF287883	AY885155	–
<i>Phlebia fuscoatra</i>	HHB-10782-Sp	United States	KP135365	KP135265	–	–

APPENDIX 1. — Continuation

Taxa	Voucher	Origin	nrITS	nrLSU	tef1a	rpb2
<i>Phlebia radiata</i>	AFTOL-ID 484	—	AY854087	AF287885	AY885156	AY218502
<i>Picipes badius</i>	Cui 11136	China	KU189812	KU189781	KU189930	KU189990
<i>Piptoporus betulinus</i>	L-15603SP	United States	KC585373	KC585202	—	—
<i>Pirex concentricus</i>	OSC-41587-Sp	United States	KP134984	KP135275	—	KP134940
<i>Polyozellus multiplex</i>	AFTOL-ID 677	—	DQ411528	AY634275	DQ028604	DQ408134
<i>Porogramme albocincta</i>	PR-1478-T	Puerto Rico	KY948725	KY948838	—	—
<i>Pycnoporus</i> sp.	CBS 355.63	Solomon Islands	AF363761	—	—	—
<i>Pycnoporus</i> sp.	CBS:326.58	Papua New Guinea	MH857801	MH869335	—	—
<i>Pycnoporus</i> sp.	148	China	JN182915	—	—	—
<i>Pycnoporus</i> sp.	186	Japan	KC525202	—	—	—
<i>Pycnoporus</i> sp.	dd08098	China	FJ810182	—	—	—
<i>Pycnoporus</i> sp.	420526MF0141	China	MH142006	—	—	—
<i>Pycnoporus</i> sp.	W006	China	AF363755	—	—	—
<i>Pycnoporus</i> sp.	034	China	EU661890	—	—	—
<i>Pycnoporus</i> sp.	420526MF0267	China	MH142019	—	—	—
<i>Pycnoporus</i> sp.	610723MF0005	China	KY950441	—	—	—
<i>Pycnoporus</i> sp.	610723MF0078	China	KY950508	—	—	—
<i>Pycnoporus</i> sp.	7IV2/1	Thailand	GQ982885	—	—	—
<i>Pycnoporus</i> sp.	7IV2/2	Thailand	GQ982886	—	—	—
<i>Pycnoporus</i> sp.	8R_1_2	Thailand	FJ372672	—	—	—
<i>Pycnoporus</i> sp.	BCC26410	Thailand	BCC26410	—	—	—
<i>Pycnoporus</i> sp.	BRFM<FRA>:6	China	JN645091	—	—	—
<i>Pycnoporus</i> sp.	CBS 356.63	Solomon Islands	AF363760	—	—	—
<i>Pycnoporus</i> sp.	CBS:376.52	Japan	MH857087	—	—	—
<i>Pycnoporus</i> sp.	CIRM-BRFM 542	—	FJ234200	—	—	—
<i>Pycnoporus</i> sp.	Cui 6980	China	KX880627	KX880665	KX880883	—
<i>Pycnoporus</i> sp.	Cui 7091	China	KX880628	—	—	—
<i>Pycnoporus</i> sp.	Cui 7096	—	KC848330	—	—	—
<i>Pycnoporus</i> sp.	CIRM-BRFM 942	Vietnam	FJ234201	—	—	—
<i>Pycnoporus</i> sp.	CIRM-BRFM 980	France	FJ234203	—	—	—
<i>Pycnoporus</i> sp.	FCG-1904	Japan	LC415498	—	—	—
<i>Pycnoporus</i> sp.	FCG-1954	Japan	LC415548	—	—	—
<i>Pycnoporus</i> sp.	FCG-1960	Japan	LC415554	—	—	—
<i>Pycnoporus</i> sp.	FCL199	—	JF308951	—	—	—
<i>Pycnoporus</i> sp.	FCL229	—	JF308952	—	—	—
<i>Pycnoporus</i> sp.	G05	China	AF363773	—	—	—
<i>Pycnoporus</i> sp.	G53	China	AF363763	—	—	—
<i>Pycnoporus</i> sp.	G66	China	AF363762	—	—	—
<i>Pycnoporus</i> sp.	H2008	China	AF363771	—	—	—
<i>Pycnoporus</i> sp.	H2180	China	AF363770	—	—	—
<i>Pycnoporus</i> sp.	HFJAU0403	China	MN258679	—	—	—
<i>Pycnoporus</i> sp.	IMB G05.10	China	FJ750267	—	—	—
<i>Pycnoporus</i> sp.	IUM0032	Korea	KP255836	—	—	—
<i>Pycnoporus</i> sp.	IUM0049	Korea	KP255840	—	—	—
<i>Pycnoporus</i> sp.	IUM0253	Korea	KP255839	—	—	—
<i>Pycnoporus</i> sp.	IUM0450	Korea	KP255837	—	—	—
<i>Pycnoporus</i> sp.	IUM0470	Korea	KP255838	—	—	—
<i>Pycnoporus</i> sp.	IUM4093	Korea	KP255841	—	—	—
<i>Pycnoporus</i> sp.	IUM4209	Korea	KP255835	—	—	—
<i>Pycnoporus</i> sp.	KKUPN2	Thailand	KU202742	—	—	—
<i>Pycnoporus</i> sp.	JZ2	India	MG273728	—	—	—
<i>Pycnoporus</i> sp.	KKUPN1	Thailand	KU202741	—	—	—
<i>Pycnoporus</i> sp.	KKUPN2	Thailand	KU202742	—	—	—
<i>Pycnoporus</i> sp.	Lu 10080720	China	KU341719	—	—	—
<i>Pycnoporus</i> sp.	M66	China	HM595574	—	—	—
<i>Pycnoporus</i> sp.	MHHNU 30644	China	MK182309	—	—	—
<i>Pycnoporus</i> sp.	MUCL 38527	Japan	FJ750266	—	—	—
<i>Pycnoporus</i> sp.	MX5	China	KF513166	—	—	—
<i>Pycnoporus</i> sp.	Não relatado	China	KJ850206	—	—	—
<i>Pycnoporus</i> sp.	NW580	China	EU520116	—	—	—
<i>Pycnoporus</i> sp.	PsFZ	China	MT879416	MT879455	—	—
<i>Pycnoporus</i> sp.	SYBC-L13	—	HQ891297	—	—	—
<i>Pycnoporus</i> sp.	SYBC-L7	—	HQ891291	—	—	—
<i>Pycnoporus</i> sp.	Thongkred 015 BCU	Thailand	JF792520	—	—	—
<i>Pycnoporus</i> sp.	W006-2	China	AF363754	—	—	—
<i>Pycnoporus</i> sp.	W3008	China	AF363753	—	—	—
<i>Pycnoporus</i> sp.	WML 2021-5-7	—	OK586736	OK586665	—	—
<i>Pycnoporus</i> sp.	WQGY2021-5-49	—	OK586749	OK586685	—	—
<i>Pycnoporus</i> sp.	ZRL2015009	China	LT716078	—	KY419090	KY419040
<i>Pycnoporus cinnabarinus</i>	DHS97_310	China	KF573022	—	—	—

APPENDIX 1. — Continuation

Taxa	Voucher	Origin	nrITS	nrLSU	tef1a	rpb2
<i>Pycnoporus cinnabarinus</i>	8R_1_1	Thailand	FJ372671	FJ372693	—	—
<i>Pycnoporus cinnabarinus</i>	APBP012	United States	MK982205	—	—	—
<i>Pycnoporus cinnabarinus</i>	BHI-F398a	United States	MF161246	—	—	—
<i>Pycnoporus cinnabarinus</i>	BRFM<FRA>:137	France	JN645086	—	—	—
<i>Pycnoporus cinnabarinus</i>	CBS:373.34	Belgium	MH855574	—	—	—
<i>Pycnoporus cinnabarinus</i>	CBS:374.34	Belgium	MH855575	MH867080	—	—
<i>Pycnoporus cinnabarinus</i>	CB :375.34	Belgium	MH855576	MH867081	—	—
<i>Pycnoporus cinnabarinus</i>	CIRM-BRFM 137	Finland	AF363757	—	—	—
<i>Pycnoporus cinnabarinus</i>	CIRM-BRFM 237	Russia	FJ234205	—	—	—
<i>Pycnoporus cinnabarinus</i>	CIRM-BRFM 945	France	FJ234206	—	—	—
<i>Pycnoporus cinnabarinus</i>	CLZhao 2434	China	MK795188	—	—	—
<i>Pycnoporus cinnabarinus</i>	Dai 14386	China	KX880629	KX880667	KX880885	—
<i>Pycnoporus cinnabarinus</i>	Dai 14867	China	KX880630	—	—	—
<i>Pycnoporus cinnabarinus</i>	HLJU418	—	KC920825	—	—	—
<i>Pycnoporus cinnabarinus</i>	I-937	Finland	AF363772	—	—	—
<i>Pycnoporus cinnabarinus</i>	JZB2115006	China	JQ293097	—	—	—
<i>Pycnoporus cinnabarinus</i>	KA16-0634	Kyrgyzstan	MK351717	—	—	—
<i>Pycnoporus cinnabarinus</i>	KA16-1036	Kyrgyzstan	MK351675	—	—	—
<i>Pycnoporus cinnabarinus</i>	KK5.4	Montenegro	KY322580	—	—	—
<i>Pycnoporus cinnabarinus</i>	M420	—	MW485554	MW520045	—	—
<i>Pycnoporus cinnabarinus</i>	MUCL 39533	—	AF363756	—	—	—
<i>Pycnoporus cinnabarinus</i>	MUCL 30555	Belgium	AF363764	—	—	—
<i>Pycnoporus cinnabarinus</i>	SWFC 002434	China	MK838871	—	—	—
<i>Pycnoporus cinnabarinus</i>	WD741	Japan	AB735965	AB735945	—	—
<i>Pycnoporus cinnabarinus</i>	ZW02.30	—	DQ411525	AY684160	DQ028600	—
<i>Pycnoporus coccineus</i>	CBS:311.33	Australia	MH855446	—	—	—
<i>Pycnoporus coccineus</i>	MUCL 38420	Australia	AF363768	—	—	—
<i>Pycnoporus coccineus</i>	MUCL 38480	Austria	AF363767	—	—	—
<i>Pycnoporus coccineus</i>	MUCL 38523	Australia	FJ873395	—	—	—
<i>Pycnoporus coccineus</i>	MUCL 38525	Australia	FJ234207	—	—	—
<i>Pycnoporus coccineus</i>	MUCL:38525	Australia	JN645094	—	—	—
<i>Pycnoporus sanguineus</i>	P21	Argentina	MF314444	—	—	—
<i>Pycnoporus sanguineus</i>	105F16C-AM	Brazil	MG751232	—	—	—
<i>Pycnoporus sanguineus</i>	4P6/1	Thailand	GQ982884	—	—	—
<i>Pycnoporus sanguineus</i>	A5	Argentina	KF850154	—	—	—
<i>Pycnoporus sanguineus</i>	A7	Argentina	KF850155	—	—	—
<i>Pycnoporus sanguineus</i>	BPLMBT2	India	KC243780	—	—	—
<i>Pycnoporus sanguineus</i>	BRFM 1114	French Guiana	JX082366	—	—	—
<i>Pycnoporus sanguineus</i>	BRFM 981	France	JX082343	—	—	—
<i>Pycnoporus sanguineus</i>	71C030	Taiwan	JN003682	—	—	—
<i>Pycnoporus sanguineus</i>	CBS 358.63	India	AF363759	—	—	—
<i>Pycnoporus sanguineus</i>	CBS:614.73	Sri Lanka	MH860781	—	—	—
<i>Pycnoporus sanguineus</i>	CFMR:6818	Puerto Rico	KX065964	—	—	—
<i>Pycnoporus sanguineus</i>	CIRM-BRFM 881	Venezuela	FJ234197	—	—	—
<i>Pycnoporus sanguineus</i>	CIRM-BRFM 892	French Guiana	FJ234185	—	—	—
<i>Pycnoporus sanguineus</i>	CIRM-BRFM 893	French Guiana	FJ234186	—	—	—
<i>Pycnoporus sanguineus</i>	CIRM-BRFM 895	French Guiana	FJ234187	—	—	—
<i>Pycnoporus sanguineus</i>	CIRM-BRFM 896	French Guiana	FJ234188	—	—	—
<i>Pycnoporus sanguineus</i>	CIRM-BRFM 898	French Guiana	FJ234189	—	—	—
<i>Pycnoporus sanguineus</i>	CIRM-BRFM 899	French Guiana	FJ234190	—	—	—
<i>Pycnoporus sanguineus</i>	CIRM-BRFM 900	French Guiana	FJ234191	—	—	—
<i>Pycnoporus sanguineus</i>	CIRM-BRFM 901	French Guiana	FJ234192	—	—	—
<i>Pycnoporus sanguineus</i>	CIRM-BRFM 902	French Guiana	FJ234193	—	—	—
<i>Pycnoporus sanguineus</i>	CIRM-BRFM 903	French Guiana	FJ234194	—	—	—
<i>Pycnoporus sanguineus</i>	CIRM-BRFM 905	French Guiana	FJ234195	—	—	—
<i>Pycnoporus sanguineus</i>	CIRM-BRFM 906	French Guiana	FJ234196	—	—	—
<i>Pycnoporus sanguineus</i>	CIRM-BRFM 943	Vietnam	FJ234202	—	—	—
<i>Pycnoporus sanguineus</i>	CIRM-BRFM 979	France	FJ234184	—	—	—
<i>Pycnoporus sanguineus</i>	CIRM-BRFM 981	France	FJ234204	—	—	—
<i>Pycnoporus sanguineus</i>	CLZhao 1104	China	MH114878	—	—	—
<i>Pycnoporus sanguineus</i>	CLZhao 4234	China	MK269185	—	—	—
<i>Pycnoporus sanguineus</i>	CLZhao 4807	China	MK269258	—	—	—
<i>Pycnoporus sanguineus</i>	CLZhao 4814	China	MK269257	—	—	—
<i>Pycnoporus sanguineus</i>	CLZhao 977	China	MH114877	—	—	—
<i>Pycnoporus sanguineus</i>	CM1	Thailand	JF792519	—	—	—
<i>Pycnoporus sanguineus</i>	CR35	Venezuela	JN164981	—	—	—
<i>Pycnoporus sanguineus</i>	CSIRO(M) E7068	Indonesia	AJ537498	—	—	—
<i>Pycnoporus sanguineus</i>	CSIRO(M) E7356	Indonesia	AJ537499	—	—	—
<i>Pycnoporus sanguineus</i>	Cui8015	—	KC848329	KC848413	—	—
<i>Pycnoporus sanguineus</i>	extr28	Taiwan	MH608343	—	—	—

APPENDIX 1. — Continuation

Taxa	Voucher	Origin	nrITS	nrLSU	<i>tef1a</i>	<i>rpb2</i>
<i>Pycnoporus sanguineus</i>	F3	—	MK168589	—	—	—
<i>Pycnoporus</i> sp.	F7	—	MK168587	—	—	—
<i>Pycnoporus</i> sp.	GQ402826	—	GQ402826	—	—	—
<i>Pycnoporus</i> sp.	HP1	Philippines	MF377427	—	—	—
<i>Pycnoporus</i> sp.	HP3	Philippines	MF377426	—	—	—
<i>Pycnoporus</i> sp.	IQ145	Peru	KJ831864	—	—	—
<i>Pycnoporus</i> sp.	JUBF18	India	MK880290	—	—	—
<i>Pycnoporus</i> sp.	KF1	Argentina	KF850158	—	—	—
<i>Pycnoporus</i> sp.	M0138530	Papua New Guinea	KF573026	—	—	—
<i>Pycnoporus</i> sp.	CIAR 37	Argentina	KF850157	—	—	—
<i>Pycnoporus</i> sp.	KU-RNB013	Thailand	LC190467	—	—	—
<i>Pycnoporus</i> sp.	L1	Argentina	KF850156	—	—	—
<i>Pycnoporus</i> sp.	LAC-01	China	KP723552	—	—	—
<i>Pycnoporus</i> sp.	M0138528	Papua New Guinea	KF573025	—	—	—
<i>Pycnoporus</i> sp.	MEL:2382627	Australia	KP012989	—	—	—
<i>Pycnoporus cinnabarinus</i>	MEL:2382815	Australia	KP012695	—	—	—
<i>Pycnoporus cinnabarinus</i>	MUCL 29375	Madagascar	AF363769	—	—	—
<i>Pycnoporus sanguineus</i>	MUCL:29375	Madagascar	JN645089	—	—	—
<i>Pycnoporus sanguineus</i>	MH225776	Vietnam	MH225776	—	—	—
<i>Pycnoporus sanguineus</i>	OAB0088	Benim	MK736969	MK736949	—	—
<i>Pycnoporus sanguineus</i>	PRSC95	Puerto Rico	JN164982	JN164795	JN164897	—
<i>Pycnoporus sanguineus</i>	SWFC 010766	China	MK894097	—	—	—
<i>Pycnoporus sanguineus</i>	Thongkred 013 BCU	Thailand	JF792517	—	—	—
<i>Pycnoporus sanguineus</i>	Thongkred 014 BCU	Thailand	JF792518	—	—	—
<i>Pycnoporus sanguineus</i>	U13-4	Brazil	MG211680	—	—	—
<i>Pycnoporus sanguineus</i>	UOC KAUNP MK53	Sri Lanka	KR348865	—	—	—
<i>Pycnoporus sanguineus</i>	UOC SIGWI S19	Sri Lanka	KP780432	—	—	—
<i>Pycnoporus puniceus</i>	BCC26408	Thailand	FJ372685	—	—	—
<i>Pycnoporus puniceus</i>	BCC27595	Thailand	FJ372686	—	—	—
<i>Pycnoporus puniceus</i>	CIRM-BRFM 1868	—	OL957167	—	—	—
<i>Pycnoporus puniceus</i>	IRET45	Africa	KY449389	—	—	—
<i>Pycnoporus puniceus</i>	MEL:2382626	Australia	KP012988	—	—	—
<i>Pycnoporus puniceus</i>	MUCL 47087	Cuba	FJ234199	—	—	—
<i>Rhodofomitopsis feei</i>	Oinonen 6011906	—	KC844851	KC844856	KR610671	KR610767
<i>Rigidoporus undatus</i>	Miettinen-13591	Finland	KY948731	KY948870	—	KF007968
<i>Sarcodon joeides</i>	REB-270	United States	KC571772	—	—	—
<i>Sarcodontia crocea</i>	OMC-1488	United States	KY948798	KY948903	—	—
<i>Scopuloides rimosa</i>	RLG-5104	United States	KP135351	KP135283	—	KP134904
<i>Sparsitubus nelumbiformis</i>	Cui 8497	China	KX880631	KX880670	KX880887	KX880856
<i>Terana caerulea</i>	FP-104073	United States	KP134980	KP135276	—	KP134960
<i>Thelephora ganbajun</i>	ZRL20151295	China	LT716082	KY418908	KY419093	KY419043
<i>Theleporus minisporus</i>	Dai 12011	China	NR119986	KX880675	KX880891	—
<i>Tinctoporellus epimiltinus</i>	CRM-55	Venezuela	KY948837	KY948720	—	—
<i>Tomentella</i> sp.	AFTOL ID 1016	United States	DQ835998	DQ835997	—	DQ835999
<i>Tomophagus colossus</i>	TC-02 (TNM)	—	KJ143923	—	KJ143943	—
<i>Trametes versicolor</i>	ZRL20151477	China	LT716079	KY418903	KY419091	KY419041
<i>Trametopsis cervina</i>	TJV_93_216T	United States	JN165020	JN164796	JN164882	JN164877
<i>Trametes polyzona</i>	Cui 11040	China	KR605824	KR605767	KR610760	KR610849
<i>Ungulidaedalea fragilis</i>	Cui 10919	China	KF937286	KF937290	KR610674	KR610770
<i>Vanderbylia robinioiphila</i>	Dai 7182	China	KX081123	KX081173	KX880921	KX880872
<i>Wolfiporia dilatohypha</i>	CS-635913	United States	KC585234	KC585234	—	—