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Rickenella fibula (Repetobasidiaceae: Basidiomycota): a tiny species with large distribution also occurs in Brazil

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ABSTRACT – During a survey of macrofungi in Santa Catarina state, Brazil, some specimens of bryophilous fungi were collected. The specimens were identified as *Rickenella fibula*, representing the first record of the species from the Brazilian Atlantic Forest. The species is characterized by bright orange basidiomata, pileus 3–5 mm in diameter, 13–20 lamellae and 1–2 lamellulae between each lamella, basidiospores ellipsoid, 4.8–7.2 × 2.0–3.3 µm and cystidia 36.5–51.1 × 5.2–8.4 µm. A morphological description, macro and microscopic photographs, as well as a distribution map of the species in South America, and a phylogenetic discussion are provided.

Keywords: Atlantic Forest, Funga, Hymenochaetales, *Rickenella* clade.

RESUMO – ***Rickenella fibula* (Repetobasidiaceae: Basidiomycota): uma pequena espécie com ampla distribuição também ocorre no Brasil.** Durante coletas de macrofungos no estado de Santa Catarina, Brasil, alguns espécimes de fungos briófilos foram coletados. Estes foram identificados como *Rickenella fibula*, representando dessa forma, o primeiro registro da espécie na Mata Atlântica brasileira. Caracteriza-se pelos basidiomas alaranjados, píleos com 3–5 mm de diâmetro, 13–20 lamelas com 1–2 lamélulas entre cada lamela, basidiósporos elipsóides com 4.8–7.2 × 2.0–3.3 µm e cistídios com 36.5–51.1 × 5.2–8.4 µm. Uma descrição macro e micromorfológica, fotografias destas estruturas, um mapa de distribuição desta espécie na América do Sul e a filogenia desta espécie são aqui discutidas.

Palavras-chave: Funga, Hymenochaetales, Mata Atlântica, *Rickenella* clade.

INTRODUCTION

Bryophilous fungi are diverse and understudied (Felix 1988, Hawksworth 2001, Davey & Currah 2006). There are about 400 species of these fungi described worldwide, most of them Ascomycota from the temperate Northern Hemisphere (Döbbeler 1997, Ptaszynska *et al*. 2009). Additionally, there are few species of bryophilous in Basidiomycota (Kost 1988), and the great majority of the studies on these species are exclusively from temperate Europe and North America (Latha *et al*. 2015).

One of the most known and studied genera of bryophilous in Basidiomycota is *Rickenella* Raithelh. (Raithelhuber 1973). Due to its classic agaric morphology, *Rickenella* was previously treated in the Agaricales Underw. (Redhead *et al*. 2002), but molecular phylogenies placed the genus in Hymenochaetales Oberw. (Moncalvo *et al*. 2000, 2002, Redhead *et al*. 2002). At the family level, the group was placed in Rickenellaceae Vizzini (Vizzini 2010, Nakasone & Burdsall 2012), an illegitimate name, and finally in Repetobasidiaceae Jülich (Jülich 1981).

This is a globally distributed genus, which can be recognized by its small omphalinoid basidiomata, bright-colored pileus, and solitary cystidia on the cap, stipe, and hymenium (Raithelhuber 1973, Pegler 1986). This combination of macro and microscopic characteristics in addition to the bryophilous habit is unique for this genus. *Blasiphalia* Redhead, another bryophilous genus, is morphologically very similar, differing by its clustered cystidia in the cap and the stipe (Smith 1947, Larsson *et al*. 2006).

According to Larsson *et al*. (2006), *Rickenella* forms the *Rickenella* clade, along with the genera *Alloclavaria* Dentinger & D.J. McLaughlin, *Cantharellopsis* Kuyper, *Contumyces* Redhead, Moncalvo, Vilgalys & Lutzoni, *Cotylidia* P. Karst., *Gyroflexus* Raithelh., *Loreleia* Redhead, Moncalvo, Vilgalys & Lutzoni, and *Muscinupta* Redhead, Lücking & Lawrey. The monophyly of *Rickenella* clade sensu Larsson *et al*. (2006) was not fully supported by Korotkin *et al*. (2018), which proposed the exclusion of some taxa treated within this clade.

Due to its bryophilous habit on apparently healthy gametophytes of mosses, the nutritional mode of *Rickenella*

has intrigued researchers for decades. Kost (1988) suggested that *R. fibula* is a parasite on mosses' rhizoids, whereas Bresinsky & Schötz (2006) considered *R. fibula* as a saprotroph, but could not dismiss an "endomycorrhizal" ecology. Korotkin *et al*. (2018) provides an extensive analysis concerning nutritional modes in Hymenochaetales and presents consistent evidence that *R. fibula* has multiple nutritional modes, such as ectomycorrhizal-like, parasitic or endophytic, and infrequently saprotrophic.

Knowledge about *Rickenella* in Brazil is very scarce, being restricted to a mention of *R. fibula* in the Pampa biome (Sulzbacher *et al*. 2018). To improve the knowledge of bryophilous fungi in Brazil, we present a new record of *R. fibula f*or the Brazilian Atlantic Forest domain, including a morphological description, *in situ* and microscopic photographs, as well as a phylogenetic discussion.

MATERIAL AND METHODS

Sampling and morphological studies

Samples were collected or observed in 2019 and 2020 in four localities: Santa Bárbara, in Parque Nacional de São Joaquim (15°10'S–15°30'S and 55°45'W–56°00'W) in Urubici, and Bom Jardim da Serra municipality, Serra do Corvo Branco in Grão Pará municipality and Vale da Liberdade, in Benedito Novo municipality (no specimen collected), all in Santa Catarina state. The studied sites are characterized by high-altitude montane areas, between 800–1200 m above sea level, with a marked seasonal climate with rainy summers and dry winters (Peel *et al*. 2007). Microscopic examinations and measurements were done using Melzer's reagent, 1 % phloxine, and 3–5 % KOH. Melzer's reagent was used to check dextrinoid and amyloid reactions. To determine the size range of the basidiospores, 5 % of the measurements at each end of the range are given in parentheses, when relevant (differing from the rest of the range), and forty of each microstructure of each specimen were measured. In the text, the following abbreviations are used: ave = arithmetic mean, Q = the ratio of length/width of basidiospores, and ave-Q = arithmetic mean of the ratio Q.

DNA extraction, PCR amplification, and sequencing

Genomic DNA was extracted from dried basidiomata following the protocol of Doyle and Doyle (1987) modified by Góes-Neto *et al*. (2005). Primer pairs ITS8-F / ITS6-R (Dentinger *et al*. 2010) were used to amplify the Internal Transcribed Spacer (ITS). PCR was performed in a total volume of 25 µL containing 4 µL of diluted DNA, 6 µL of ultrapure Milli-Q water, 13 µL of Master Mix (Promega), and 1 µL of each primer (10 pmol / L). The obtained amplicons were purified according to protocol with 20 % Polyethylene Glycol (PEG) (Sambrook *et al*. 1989). Afterward, the samples were analyzed on an agarose gel prepared in the proportions of 36 mL of TBE buffer (Tris / Borate / EDTA) and 0.288 g of ultrapure agarose (UltraPure ™ Agarose). In each well of the gel, 2 µL of the sample was added together with 2 µL of the 1 kb molecular mass marker (DNA ladder) to indirectly estimate the amount and concentration of DNA through single bands in the samples, revealed by UV Transilluminator. The purified amplification products were sequenced by the Sanger method in an automatic sequencer using 20 to 30 ng of DNA for every 100 bp of the sample. The samples were sequenced by capillary electrophoresis in an ABI3730 device, using polymer POP7 and BigDye v3.1.

Phylogenetic analyses

One dataset composed of our sequences and all the sequences of *Ricknella* available in Genbank (excluding sequences without specific identification and from environmental samples) was constructed (Tab. 1). *Cotylidia undulata* (Fr.) P. Karst. and *Cyphellostereum laeve* (Fr.) D.A. Reid were used as the outgroup based on Zhang *et al.* (2018). The dataset was aligned using MAFFT 7 (Katoh *et al.* 2017), and the alignments were manually inspected and adjusted using MEGA 6 (Tamura *et al.* 2013). We used Partition Finder v.2 (Lanfear *et al*. 2016) to estimate the best-fit partitioning strategy and the best-fit model of nucleotide evolution for the dataset using 3 data blocks (ITS1, 5.8S, ITS2).

Bayesian Inference (BI) and Maximum Likelihood (ML) phylogenetic analyses were applied to the dataset. BI was performed using defined partitions and evolutionary models in MrBayes 3.2 (Ronquist *et al*. 2012) with two independent runs, each one beginning from random trees with four simultaneous independent chains, for 107 generations, sampling parameters every 1000 generations and using the stoprule command with the value of stopval set to 0.01. The first 25 % of sampled trees were discarded as burn-in, while the remaining ones were used to reconstruct a 50 % majority-rule consensus tree and calculate Bayesian posterior probabilities (BPP) of the clades. ML searches were conducted with RAxML-HPC 8.2.3 (Stamatakis 2014). The analysis initially involved 100 ML searches, each one starting from one randomized stepwise addition parsimony tree, under a GTRGAMMA model, with all the other parameters estimated by the software. Multiparametric bootstrapping replicates under the same model were computed, allowing the program to halt bootstrapping automatically by the autoMRE option. An additional alignment partition file to force RAxML software to search for a separate evolution model for each partition was used. PartitionFinder v.2, MrBayes 3.1.2, and RAxML-HPC 8.2.3 were performed in the CIPRES science gateway (Miller *et al*. 2010, http://www.phylo.org/). The final alignment and the retrieved topologies were deposited in TreeBASE (http://www.treebase.org), under accession 27092 (http://purl.org/phylo/treebase/phylows/study/TB2:S27092?x-access-code=2801ba9dfe6e325fe2bcdd08350c7b4d&format=html). The sequences treated as R. fibula in the final topology were projected in a world map according to its occurrence using the function phylo.to.map of Phytools package (Revell 2012) in R (R Core Team 2020) and visual editing in CorelDRAW 11.

Table 1. Species, vouchers, localities, and accession numbers of the specimens used in phylogenetic analyses.

Species	Voucher	Locality	GenBank
Cyphellostereum laeve	JJ 020909	Sweden	EU118621
Cotylidia undulata	Olsson011101	Sweden	JN649335
Rickenella danxiashanensis	GDGM45513	China	MF326424
Rickenella danxiashanensis	GDGM45529	China	MF326425
Rickenella danxiashanensis	GDGM45576	China	MF326426
Rickenella danxiashanensis	GDGM45679	China	MF326427
Rickenella fibula		Brazil	FB1278
Rickenella fibula		Brazil	LF8948
Rickenella fibula	PBM2503	–	DQ241782
Rickenella fibula	GG154_88	–	GU234163
Rickenella fibula	PDD:95782	New Zealand	JQ694100
Rickenella fibula	Champ-60	France	KX449464
Rickenella fibula	MES950	Chile	KY559313
Rickenella fibula	HBK012	United States	MF319080
Rickenella fibula	HBK014	United States	MF319082
Rickenella fibula	HBK015	United States	MF319083
Rickenella fibula	H:6019327	Finland	MF319088
Rickenella fibula	H:6034921	Finland	MF319089
Rickenella fibula	H:6034922	Finland	MF319090
Rickenella fibula	H:6059291	Finland	MF319091
Rickenella fibula	H:6059302	Finland	MF319092
Rickenella fibula	PBM2506	United States	MF319093
Rickenella fibula	GDGM42134	China	MG760850
Rickenella fibula		Mexico	MH285338
Rickenella fibula	MHHNU 7907	–	MK172820
Rickenella fibula	HFJAU ND072	China	MN622764
Rickenella indica	K(M) 190585	India	KJ187769
Rickenella indica	K:190585	India	NR_137857
Rickenella mellea	BSI 13/255	Switzerland	KR606033
Rickenella mellea	CBS 579.87	France	MH862106
Rickenella mellea	CBS 581.87	France	MH862107
Rickenella minuta	MES1950	Argentina	KY559314
Rickenella minuta	MES1891	Argentina	KY559315
Rickenella minuta	MES1054	Chile	KY559319
Rickenella minuta	MES1558	Chile	KY559320
Rickenella swartzii (as *R. setipes*)	GG119_88	–	GU234136
Rickenella swartzii (as *R. setipes*)	P. Salo 4860	Finland	MF319109
Rickenella swartzii (as *R. setipes*)	R. Saarenoksa 06978	Finland	MF319110
Rickenella swartzii (as *R. setipes*)	I. Kytovuori 93-032	Finland	MF319111
Rickenella swartzii	HRL1399	United States	MF319112
Rickenella swartzii	HRL1452	Canada	MF319113
Rickenella swartzii	MGW1341	United States	MF319114
Rickenella swartzii	HBK-M8.2	United States	MG982534

RESULTS

Phylogenetic analyses

The final aligned dataset contained 43 sequences, 701 characters including gaps, of which 403 are constant, 279 variable, and 178 are parsimony informative. The evolutionary selected models were HKY+G (ITS1+ITS2) and JC (5.8S). ML and BI analyses generated trees with identical topologies. Only the best-scored ML tree is shown (Fig. 1). Two major lineages were recovered in the topology: one of them is composed by *R. minuta* (Singer & Digilio) Raithelh. (1 BPP, 100 % BS), and the other (1 BPP, 98 % BS) is composed of terminal branches representing *Rickenella danxiashanensis* Ming Zhang & T.H. Li (1 BPP, 100 % BS), *R. indica* K.P.D. Latha & Manim. (1 BPP, 100 % BS), *R. swartzii* (Fr.) Kuyper (1 BPP, 100 % BS), *R. mellea* (Singer & Clémençon) Lamoure, and at least three clades with specimens identified as *R. fibula.*

Taxonomy

Rickenella fibula (Bull.) Raithelh., Metrodiana 4: 67.1973. (Figs. 2-3)

Macroscopic characters: Basidiomata small, omphalinoid. Pileus 3–4 mm diameter, hemispheric at first, becoming convex to nearly plane with a shallow central depression and slightly wavy margin in age; surface dry to hygrophanous, glabrous to the naked eye and finely pubescent under a lens, yellowish orange to orange, deep orange to brownish at the central depression. Lamellae 18–20, decurrent to deeply decurrent, furcate or transvenose, white to yellowish white, up to 2 mm wide; lamellulae 1–2 of different lengths between the two complete lamellae, edge entire, concolorous, intervenose, not to occasionally forked. Stipe central, 12–15 × 0.2–0.5 mm, cylindrical to subcylindrical, often curved, equal or slightly tapered downwards and upwards, cartilaginous, solid, white to yellowish white, somewhat translucent; surface covered with finely pubescent; basal mycelia white. Odor and taste not distinctive. Microscopic characters: Basidiospores (4.8–)5.0–6.7 × (1.6–)2.0–2.8(–3.0) µm, Q = (1.43–)1.51–1.82(–2.0), Qm = 2.3 ± 0.7, ellipsoid, thin-walled, hyaline, smooth, inamyloid. Basidia 14.5–20 × 3.6–4.3 µm, clavate, 4-spored, thin-walled; sterigmata 3.6–4 µm, often clamp connections at the base of the basidia. Pleurocystidia 36.5–51.1 × 5.2–8.4 µm, narrowly lageniform to subcapitate, often with subcapitate apex, hyaline, thin-walled, inamyloid. Cheilocystidia similar to pleurocystidia in shape and size. Lamella trama regular to subregular, hyphae 8.5–17.7 µm wide, cylindrical or subfusoid, thin-walled, hyaline, inamyloid. Pileus trama subregular, hyphae 3–12 µm wide, thin-walled, hyaline, inamyloid. Pileipellis as a cutis with scattered pileocystidia, hyphae 3–12 µm wide, cylindrical or subfusoid, thin-walled, hyaline. Pileocystidia similar to pleurocystidia in shape and size. Stipitipellis a cutis with scattered caulocystidia, hyphae 3–11 µm wide, with cylindrical elements, hyaline, thin-walled. Caulocystidia similar to pleurocystidia in shape and size. Clamp connections present.

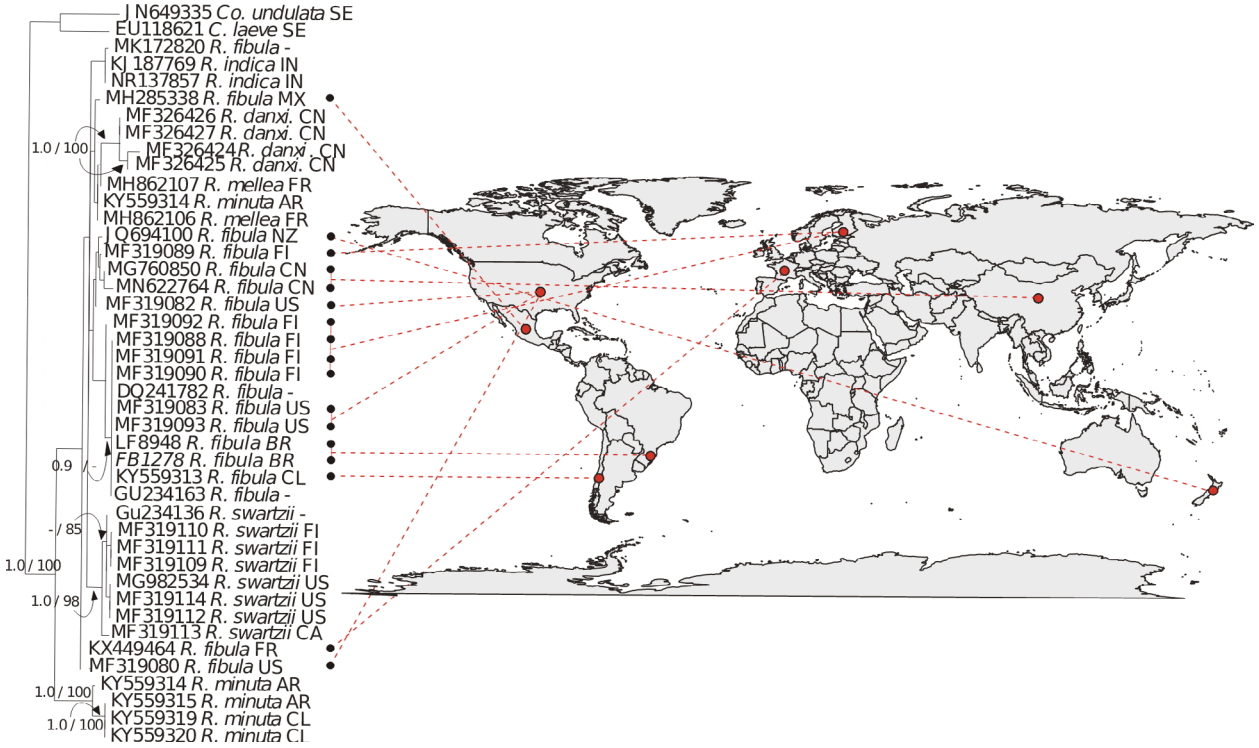

Figure 1. Maximum likelihood (ML) tree of *Rickenella* based on data set of ITS sequences. Bayesian posterior probability above 0.7 and bootstrap values above 50 % are shown. Sequences generated in this work are in bold.

Figure 2. Macroscopic characters of *Rickenella fibula*. **A.** Detail of the pileus; **B.** Detail of the stipe, showing the decurrent lamellae; **C.** Hymenophore, showing the lamellae and lamellulae.

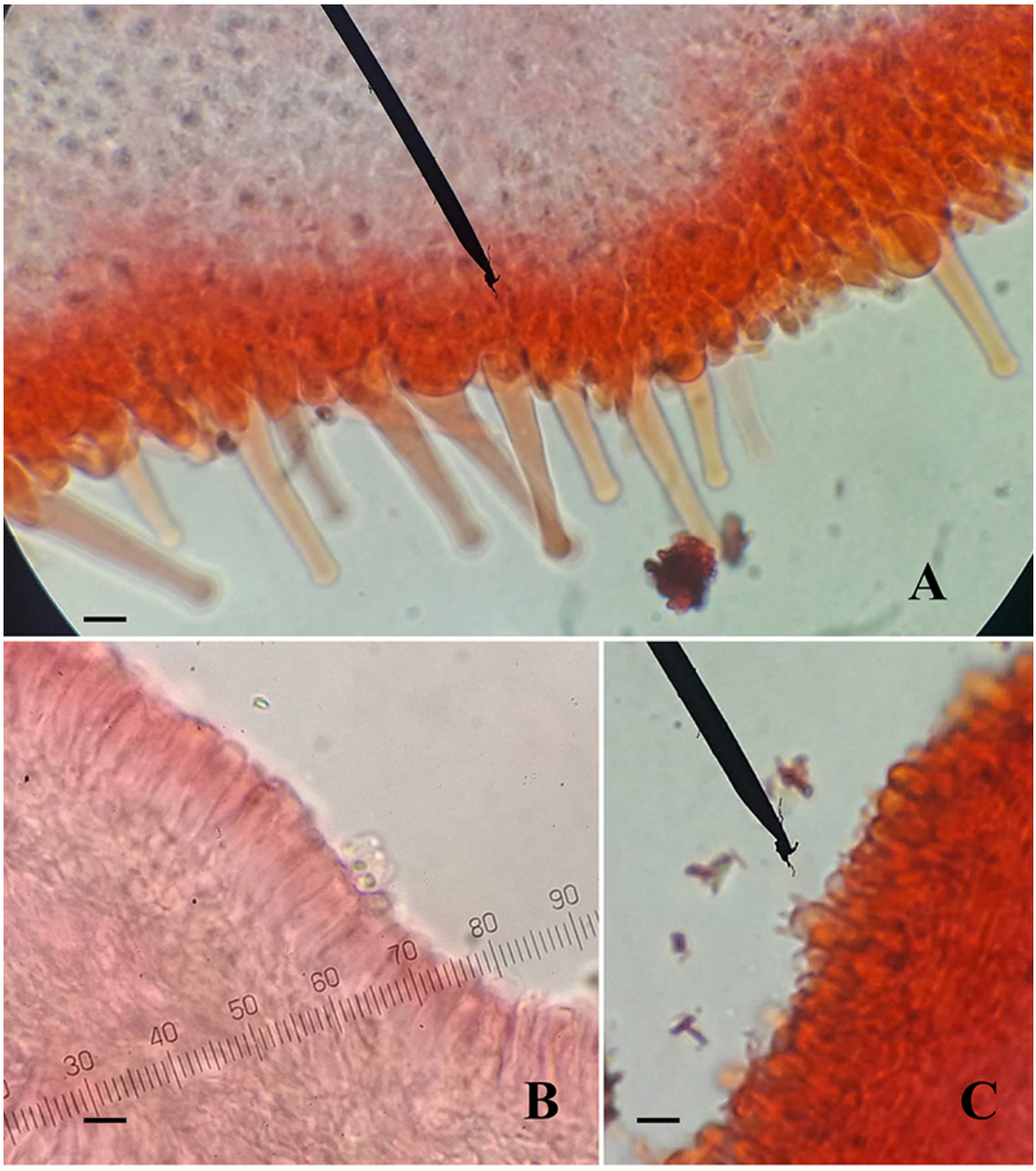

Figure 3. Microscopic characters of *Rickenella fibula*. **A.** Pleurocystidia; **B.** Basidiospores attached to the basidia; **C.** Basidia.

Specimens examined: BRAZIL, SANTA CATARINA, Grão Pará, Serra do Corvo Branco, 17.III.2020, L.A. Funez & W.I. Ribeiro-Nardes 8951 (FLOR); Urubici, Parque Nacional de São Joaquim, 01.V.2019, D.H. Costa-Rezende, L.A. Funez & M. Monteiro 584 (FLOR); Estrada geral da Santa Bárbara, 02.V.2019, L.A. Funez, M. Monteiro & D.H. Costa-Rezende 8948 (FLOR); 8949 (FLOR); 19.IX.2019, L.A. Funez, W.I. Ribeiro-Nardes & M. Comin 9097 (FLOR); 26.III.2019, L.A. Funez, T. Kossmann, D.H. Costa-Rezende & D.K.S Guimarães 9155 (FLOR); 30.I.2020, L.A. Funez, W.I. Ribeiro-Nardes & M. Comin 9422 (FLOR); 28°9'38"S, 49°37'5"W, 21.V.2019, F. Bittencourt, L.A. Funez & D.H. Costa-Rezende 1278 (FLOR).

DISCUSSION

The studied specimens fit the broad morphological circumscription of *R. fibula*, being mainly characterized by bright-orange basidiomata, pileus with 3–5 mm wide, 13–20 lamellae, and 1–2 lamellulae between two lamellae, basidiospores ellipsoid, 4.8–7.2 × 2.0–3.3 µm and cystidia 36.5–51.1 × 5.2–8.4 µm (Saccardo 1887, Singer 1943, 1970, Smith 1947, Rea 1922, Phillips 1981, Zhang *et al.* 2018, Bas *et al*. 1995, Baroni 2017, Desjardin *et al*. 2015).

Rickenella fibula is a globally distributed bryophilous agaric popularly known as "orange mosscap". The species has been recorded in all continents, along all Europe (Bas *et*

al. 1995) and North America (Bas *et al*. 1995, Baroni 2017, Desjardim *et al*. 2015), Oceania, in Australia mainland (May *et al*. 2003, Catcheside & Catcheside 2008, Bougher 2009) and Tasmania (Gates *et al*. 2005, Ratkowsky & Gates 2005), Asia, in China (Kakikawa *et al*. 2008, Zhang *et al*. 2018) and Turkey (Solak *et al*. 2003), Africa, in Kenya (Kost 2002) and few records in South America, in Chile (Valenzuela *et al*. 1996, Korotkin *et al*. 2018), Bolivia, Colombia (Singer 1970), Argentina (Singer 1970, Horak 1979, Niveiro & Albertó 2012, Korotkin *et al*. 2018), Falklands (Watling 2012), Subantarctic (Convey *et al*. 2000) and Antarctic Islands (Calonge & Pegler 1992, Horak 1980) and Brazil (Sulzbacher *et al*. 2018). However, only one of those studies (Singer 1970) presents a taxonomic approach including cited vouchers and morphological descriptions in South America.

The samples studied here are from Santa Catarina State, Brazil. *Rickenella fibula* has been mainly recorded in temperate regions around the world (Latha *et al*. 2015, Zhang *et al*. 2018). The known records from South America occur at high elevations and/or middle latitudes (Fig. 4), which are associated with mild to cold temperatures. All specimens were found inhabiting humid moss-beds of *Polytrichium* Hedw. and *Schizymenium* Harv., on exposed rocky soil and ravines at elevations about 800–1200 m a.s.l. (Fig. 5). Although numerous basidiomata were locally present in some populations, we observed that most moss beds we found in similar conditions did not present basidiomata of *R. fibula*, thus more studies are necessary to understand the required environmental, soil and biological relationships for this species establishment.

According to the phylogenetic analysis (Fig. 1), our specimens grouped in a moderately to well-supported clade (0.99 BPP / 71 % BS) including sequences identified as *R. fibula* from Chile, the United States, Finland, and Norway, which could corroborate the worldwide distribution currently recorded for *R. fibula*. However, sequences identified as *R. fibula* grouped in distinct poorly supported or unresolved clades. Also, some sequences identified as *R. fibula* grouped with *R. indica* K.P.D. Latha & Manim and *R. danxiashanensis* Ming Zhang & T.H. Li, probably representing misidentified specimens. Previous studies also retrieved multiple clades and the occurrence of misidentified sequences, or unclear phylogenetic relationships of *R. fibula* (Zhang *et al*. 2018, Korotkin *et al*. 2018). Although ITS may be appropriate for phylogenetic studies at the infrageneric level (Hyde *et al*. 2013), the lack of resolution observed might be attributed to insufficient sampling of species and genes/markers. Nevertheless, considering the broad geographic distribution and morphological concept of the taxon, as well as the phylogenetic results, future studies might point *R. fibula* as a taxonomic complex.

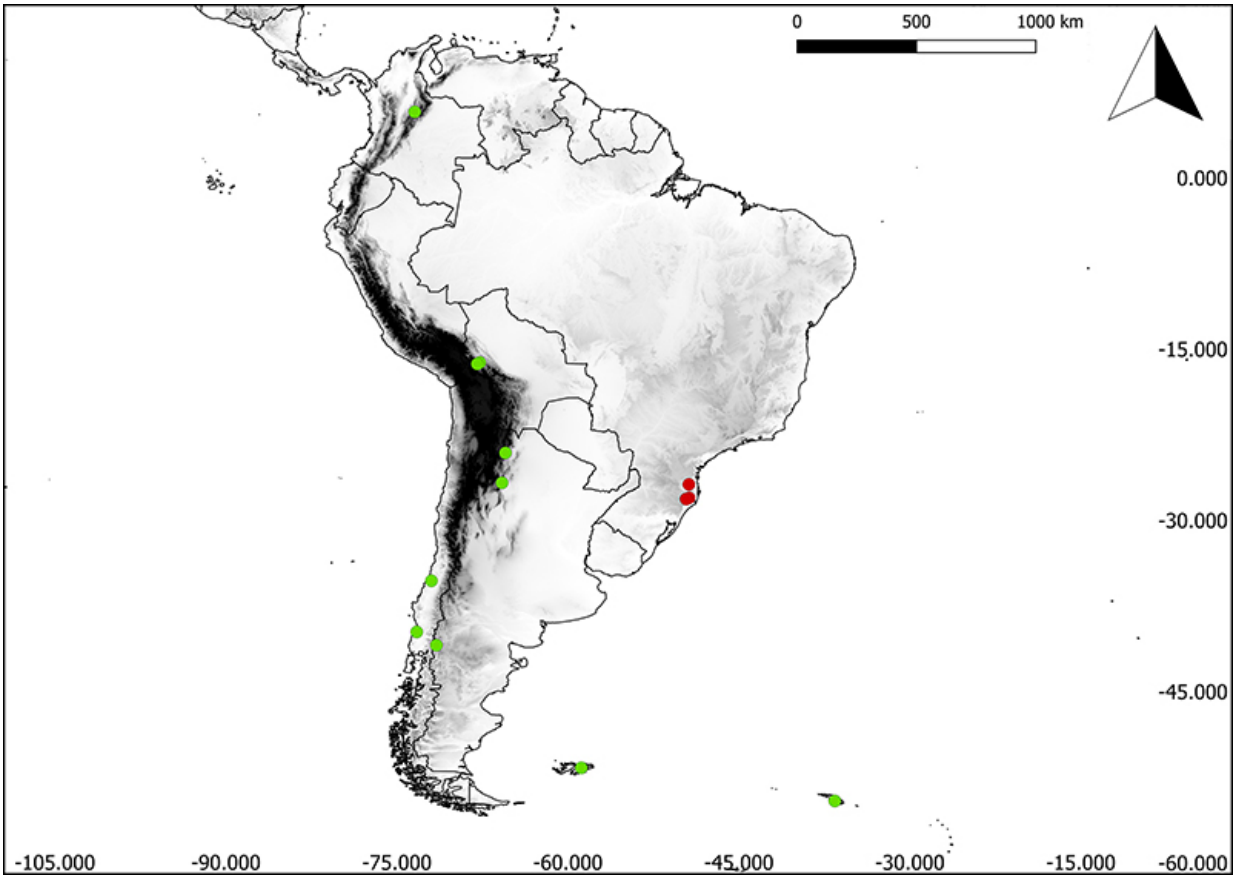

Figure 4. Distribution map of *Rickenella fibula* in South America. Green dots are previous collections and red dots are the specimens studied in this work.

Figure 5. *Rickenella fibula* in habitat. **A.** Two basidiomata in a moss bed of *Schizymenium and Polytrichum*; **B.** A basidiome (red arrow) in a ravine full of *Polytrichum* moss.

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